NATIONAL MARROW DONOR PROGRAM®

BE THE MATCH®

August 1, 2018

Lt. Cdr. Brian Andrews-Shigaki
Office Warfighter Performance S&T Dept
875 N. Randolph St.
Arlington, VA 22203-1995

Subject: Final Technical Report with SF298 by the National Marrow Donor Program®

Reference: Grant N00014-17-1-2388 between the Office of Naval Research and the National Marrow Donor Program

Dear Lt. Cdr. Andrews-Shigaki,

In accordance with the requirements of the Referenced Office of Nava Research Grant, the National Marrow Donor Program® (NMDP) hereby submits the required Final Technical Report for the period of April 1, 2017 through March 31, 2019. Please note that all expenditures for this grant were completed by March 31, 2018, and we are closing it out early. This is a final submission.

Should you have any questions regarding the performance activity of under this Grant, you may contact our Chief Medical Officer – Dennis Confer, MD directly at 763-406-3425 or dconfer@nmdp.org.

Please direct any contractual questions pertaining to the Grant to me at 763-406-3401 or to npoland@nmdp.org.

Sincerely,

Nancy R. Poland

Nancy R. Poland, M.A.
Contracts and Compliance Manager

c: Patricia Woodhoiuse – ONR-Chicago
Dr. Robert J. Hartzman, CAPT, MC, USN (Ret)
Jennifer Ng, PhD – C.W. Bill Young Marrow Donor Recruitment and Research Program
DTIC (Ste 0944)
NRL (Code 5596)
Dennis Confer, MD – NMDP
Stephen Spellman – NMDP

REPORT DOCUMENTATION PAGE

Form Approved
OMB No. 0704-0188

1. REPORT DATE *(DD-MM-YYYY)*	2. REPORT TYPE	3. DATES COVERED *(From - To,*
01-08-2018	Final Technical Report	Oct 2016 – March 2019

4. TITLE AND SUBTITLE
Development of Medical Technology for Contingency Response to Marrow Toxic Agents – Final Technical Report with SF298 October 01, 2016 to March 31, 2019.

5a. CONTRACT NUMBER
N/A

5b. GRANT NUMBER
N00014-17-1-2388

5c. PROGRAM ELEMENT NUMBER
N/A

6. AUTHOR(S)
Spellman, Stephen

5d. PROJECT NUMBER
N/A

5e. TASK NUMBER
Project 1, 2, 3, 4

5f. WORK UNIT NUMBER
N/A

7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES)
National Marrow Donor Program
500 N. 5th St.
Minneapolis, MN 55401-1206

8. PERFORMING ORGANIZATION REPORT NUMBER
N/A

9. SPONSORING/MONITORING AGENCY NAME(S) AND ADDRESS(ES)
Office of Naval Research
875 N. Randolph Street, Suite 1425
Arlington VA 22203-1995

10. SPONSOR/MONITOR'S ACRONYM(S)
ONR

11. SPONSORING/MONITORING AGENCY REPORT NUMBER
N/A

12. DISTRIBUTION AVAILABILITY STATEMENT
Approved for public release; distribution is unlimited

13. SUPPLEMENTARY NOTES
All expenditures on this Grant were completed by March 31, 2018.

14. ABSTRACT
1. Contingency Prepardness: Collect information from transplant centers, build awareness of the Transplant Center Contingency Planning Committee and educate the transplant community about the critical importance of establishing a nationwide contingency response plan.

2. Rapid Identification of Matched Donors: Increase operational efficiencies that accelerate the search process and increase patient access are key to preparedness in a contingency event.

3. Immunogenetic Studies: Increase understanding of the immunologic factors important in HSC transplantation

4. Clinical Research in Transplantation: Create a platform that facilitates multicenter collaboration and data management.

15. SUBJECT TERMS
Research in HLA Typing, Hematopoietic Stem Cell Transplantation and Clinical Studies to Improve Outcomes

16. SECURITY CLASSIFICATION OF:			17. LIMITATION OF ABSTRACT	18. NUMBER OF PAGES	19a. NAME OF RESPONSIBLE PERSON
a. REPORT	b. ABSTRACT	c. THIS PAGE			Dennis L. Confer, MD – Chief Medical Office
U	U	U		109	19b. TELEPONE NUMBER (*Include area code*) 763-406-3425

NATIONAL MARROW DONOR PROGRAM®

BE THE MATCH®

Grant Award N00014-17-1-2388

DEVELOPMENT OF MEDICAL TECHNOLOGY FOR CONTINGENCY RESPONSE TO MARROW TOXIC AGENTS

FINAL RESEARCH PERFORMANCE REPORT

SUBMITTED AUGUST 1, 2018

Office of Naval Research

And

The National Marrow Donor Program®

500 5th St N

Minneapolis, MN 55401

I. Heading

PI: Dennis L. Confer, M.D.

National Marrow Donor Program

N00014-17-1-2388

Development of Medical Technology for Contingency Response to Marrow Toxic Agents

II. Scientific and Technical Objectives

The main objective of this grant is to develop, test and mature the ability of the National Marrow Donor Program® (NMDP) to address contingency events wherein civilian or military personnel are exposed to marrow toxic agents, primarily ionizing radiation or chemical weapons containing nitrogen mustard. An accident, a military incident, or terrorist act in which a number of individuals are exposed to marrow toxic agents will result in injuries from mild to lethal. Casualties will be triaged by first responders, and those with major marrow injuries who may ultimately be candidates for hematopoietic cell transplantation (HCT) will need to be identified. HCT donor identification activities will be initiated for all potential HCT candidates. NMDP-approved transplant centers will provide a uniform and consistent clinical foundation for receiving, evaluating and caring for casualties. NMDP coordinating center will orchestrate the process to rapidly identify the best available donor or cord blood unit for each patient utilizing its state-of-the-art communication infrastructure, sample repository, laboratory network, and human leukocyte antigen (HLA) expertise. NMDP's on-going immunobiologic and clinical research activities promote studies to advance the science and technology of HCT to improve outcomes and quality of life for the patients.

III. Approach

A. Contingency Preparedness
HCT teams are uniquely positioned to care for the casualties of marrow toxic injuries. The NMDP manages a network of centers that work in concert to facilitate unrelated HCT. The Radiation Injury Treatment Network (RITN), comprised of a subset of NMDP's network centers, is dedicated to radiological disaster preparedness activities and develops procedures for response to marrow toxic mass casualty incidents.

B. Development of Science and Technology for Rapid Identification of Matched Donors
Disease stage at the time of transplantation is a significant predictor of survival, decreasing the time to identify the best matched donor is critical. Methods are under development to rapidly provide the best matched donor for HCT.

C. Immunogenetic Studies in Transplantation
Improving strategies to avoid and manage complications due to graft alloreactivity is essential to improve the outcomes of HCT. Research efforts are focused on strategies to maximize disease control while minimizing the toxicity related to alloreactivity in HCT.

D. Clinical Research in Transplantation

Clinical research creates a platform that facilitates multi-center collaboration and data management to address issues important for managing radiation exposure casualties. Advancing the already robust research capabilities of the NMDP network will facilitate a coordinated and effective contingency response.

IV. Concise Accomplishments

a. Contingency Preparedness
   i. Conducted 7 regional tabletop, 64 local tabletop, 1 full-scale and 2 functional RITN exercises.
   ii. Conducted training sessions and tracked training activities at RITN centers.
   iii. Held the semi-annual RITN Workshop titles *Radiological and Nuclear Preparedness: Operationalizing a Decade of Development*
b. Development of Science and Technology for Rapid Identification of Matched Donors
   i. Supported the HLA typing of 175,131 newly recruited U.S. donors (44% minority).
   ii. Completed analysis of the Proactive Information Session Project-Phase 2. Donors receiving the proactive intervention proceeded to workup an average of 24 days after formal search activation compared to 41 days for non-project donors.
   iii. Planned and conducted four Data Standards Hackathons (DaSH) held in Vienna, Berkeley, Heidelberg and Utrecht.
   iv. Supplied the NIH Transplant Program with 13 products (4 PBSC, 2 CBU, 5 bone marrow and 2 therapeutic T cells).
c. Immunogenetic Studies in Transplantation
   i. Completed retrospective HLA and KIR typing on 3,720 related and unrelated donor/recipient pairs.
   ii. Published a manuscript describing the allogenicity of mismatches outside the antigen recognition domain (ARD).
d. Clinical Research in Transplantation
   i. Published 115 peer reviewed manuscripts and presented 100 abstracts at national/international meetings during the grant period.

ii. Completed analysis required to integrate an electronic Patient Reported Outcomes (ePRO) system. This system will enable patients to contribute PRO data directly to clinical studies and other CIBMTR research.

iii. Implemented 5 cellular therapy form revisions and developed 3 new forms needed to support a cellular therapies registry.

V. Expanded Accomplishments

Contingency Preparedness

Recovery of casualties with significant myelosuppression following radiation or chemical exposure is optimal when care plans are designed and implemented by transplant physicians.

Hospitals are eligible to join RITN if they participate in both the NMDP Network of treatment centers and the NDMS. The NDMS is comprised of over 1,800 accredited hospitals across the nation that have agreed to receive trauma casualties following a disaster. The program is managed by the Department of Health and Human Services. RITN conducts targeted recruitment on an annual basis with a goal of expanding the network. During the grant period, one new transplant center joined RITN (University of Chicago); resulting in a total composition of: 68 transplant centers, 5 donor centers, and 6 cord blood banks (Figure 1).

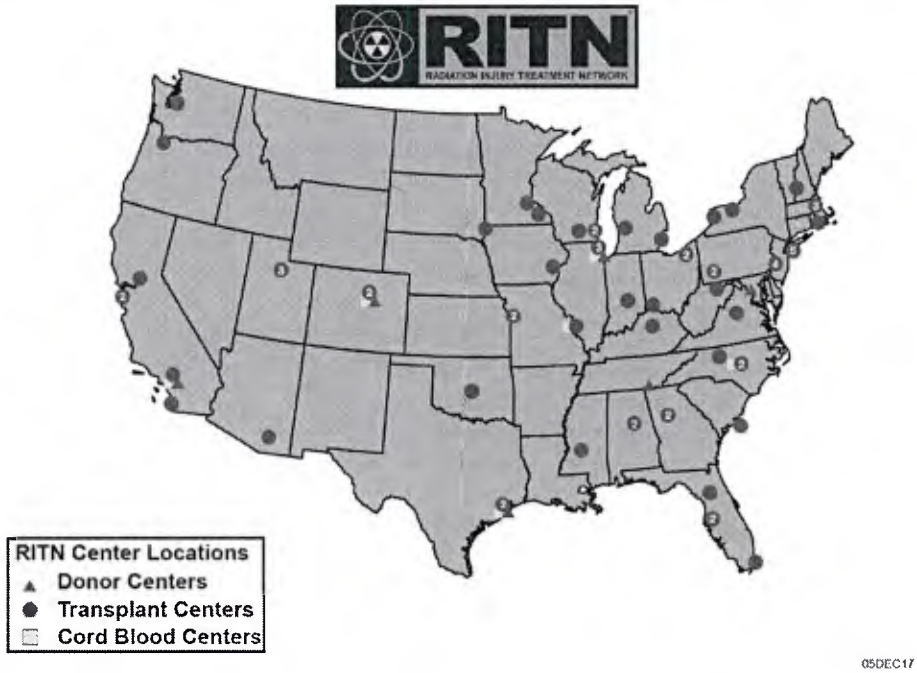


Figure 1. Location of RITN Centers

RITN Preparedness Activities

RITN centers were asked to continue to develop their level of preparedness during 2017. Tasks included communications drills, updating of standard operating procedures, outreach to local public health and emergency management contacts, a tabletop exercise and training of staff. During 2017, 100% of active RITN centers completed all of their required annual tasks (Figure 2), which is above the program lifetime average of 97%.

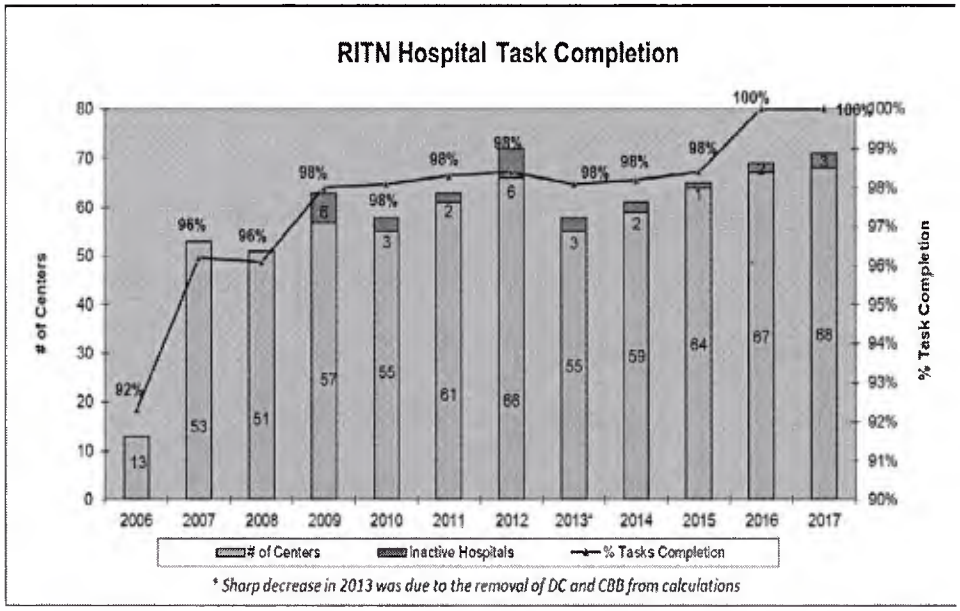


Figure 2. RITN annual training task completion rates by year

- **RITN Exercise Program:** RITN coordinates or provides support for many radiological exercises each year; these include full-scale, functional, regional tabletop and tabletop exercises (the intensity and effort required decreases accordingly from full-scale to tabletop). RITN has facilitated more than 650 exercises since 2006 (see Figure 5 for breakdown by type). During 2017 multiple radiological disaster exercises were supported across the nation. RITN coordinated and funded the following radiological disaster exercises:
    - Regional tabletop exercises at:
        - Banner University Medical Center (Tucson, AZ)

- Children's Hospital of Philadelphia (Philadelphia, PA)
- Children's Mercy Hospital (Kansas City, MO)
- Memorial Sloan-Kettering Cancer Center (NYC, NY)
- Spectrum Health (Grand Rapids, MI)
- Texas Children's (Houston, TX)
- Wake Forest Baptist Health (Winston-Salem, NC)

- Full-scale exercises in:
  - Spectrum Health (Grand Rapids, MI)
- Functional exercises in:
  - Massachusetts General Hospital (Boston, MA)
  - Rush University Medical Center (Chicago, IL)
- Annual RITN tabletop exercise conducted by 64 hospitals
  - 50 hospitals participated in one of six web based tabletop exercises that were facilitated by RITN
  - 14 hospitals facilitated the RITN exercise on their own
- After Action Reports are posted on RITN.net

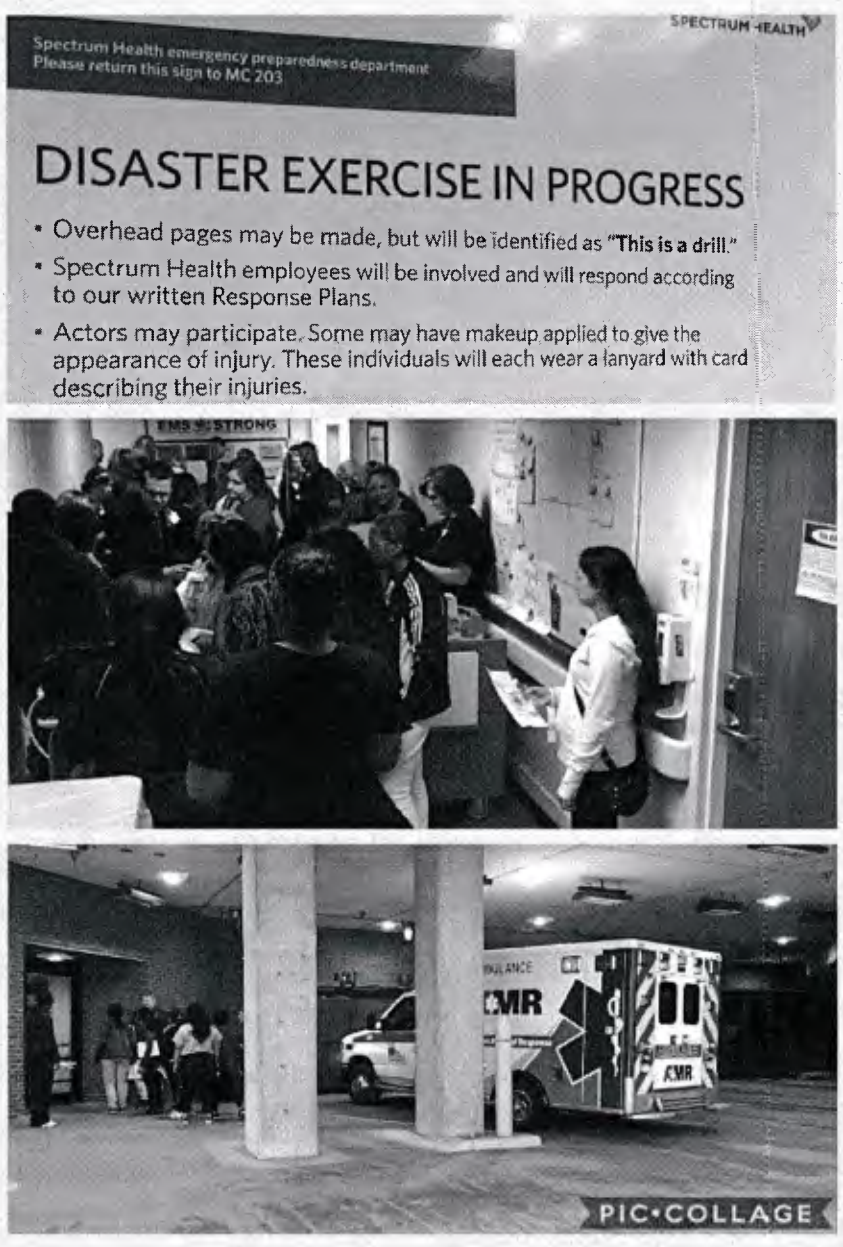


Figure 3: Images from the Spectrum Health full scale exercise 2017.

Figure 4: Images from the Rush University Medical Center Functional Exercise 2017

These exercises involved many external partners necessary for the response ranging from local public health, to emergency management, adjacent hospital, the hospital coalitions, and federal representation to name a few. Exercise planning materials and After Action Reports summarizing successes and lessons learned are publicly available on the RITN website (www.RITN.net/exercises).

Tabletop exercises: The 2017 tabletop exercise presented a scenario where a 1 kT improvised nuclear device was detonated in a metropolitan area, each hospital was asked specific questions about triage for either three adult or three pediatric patients with the

restriction that there was only one bed available (Figure 5). The number of RITN centers participating in tabletop exercises annually is summarized in Figure 5. A summary of RITN tabletop exercises conducted to date is provided in Table 1. After Action Reports from all of the 64 tabletop exercises conducted are available on the RITN website at https://ritn.net/display.aspx?id=2147484344.

Exercise Name	2017 RITN Tabletop Exercise (TTX)
Exercise Date	2017
Scope	This exercise is a distance-based tabletop exercise planned for 2 ½ hours. Exercise play is limited to RITN facilities and their response partners' collective challenges and considerations for improved and effective response.
Mission Area(s)	Response
Capabilities	Public Health & Medical Services
Objectives	**Objective 1:** Hospital staff are able to determine their hospital's capability to receive casualties (inpatient and outpatient) through the National Disaster Medical System (NDMS) following a mass casualty radiological incident. **Objective 2:** Hospital staff are able to discuss the procedures for implementing Crisis Standards of Care (CSC) at their hospital. **Objective 3:** Hospital staff are able to describe their approaches for triaging patients and determining initial treatment actions for patients with Acute Radiation Syndrome (ARS).
Hazzard	Radiological
Scenario	Medical surge from a distant radiological incident
Sponsor	Radiation Injury Treatment Network® (RITN) National Marrow Donor Program (NMDP) Office of Naval Research (ONR)

Figure 5. RITN 2017 table top exercise scenario.

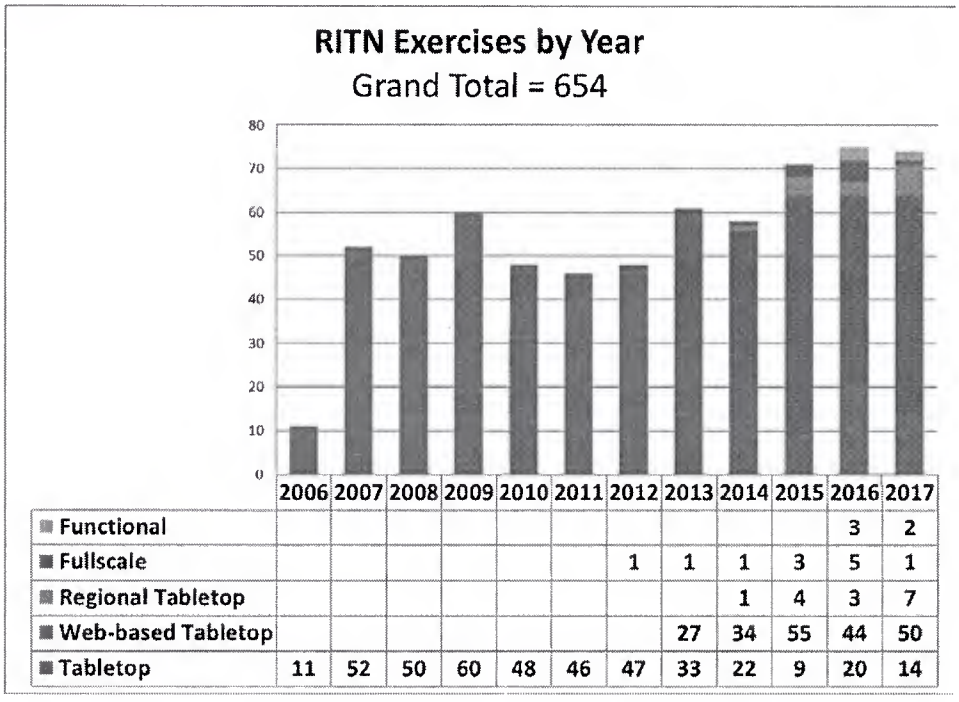


Figure 6. Number of RITN centers participating in exercises by year.

Table 1. Summary of annual RITN tabletop exercise scenarios and level of patient surge.

Summary of RITN Tabletop Exercise Scenarios		
Year	**Scenario**	**Max Victims**
2006	Radiological Exposure Device (RED) placed on public train system	650 identified as having some level of ARS. 50 patients to each center
2007	Train derailment spills multiple chemicals, produces vapor cloud which exposes a crowd of 15,000	5,000 (mostly children and senior citizens)
2008	IND was detonated and 300,000 victims were triaged	5,000 victims required RITN assistance

2009	10-kiloton nuclear device detonated in a major metropolitan center	12,000 patients with high radiation dose in the 200-600 rad range. 300 patients to each center
2010	Detonation of a surface burst 10-kiloton nuclear device in major metropolitan center	20,000 patients with high radiation dose in the 200-600 rad range. 500 patients to each center
2011	National Disaster Medical System (NDMS) flow and integration	Not specified
2012	1 KT IND detonated 500 miles away from RITN center, 20 patients to prioritize using provided casualty cards	20 casualty cards w/ limited bed availability provided
2013 w/ Webinar Option	Radiological exposure devices placed on mass transit vehicles in multiple US cities	4,500 casualties nationwide; 300 patients and 140 family members are sent to each RITN center
2014 Primarily Webinar	Detonation of a 1KT IND	100 patients from a large metropolitan area 500 miles away
2015 Primarily Webinar	Four Radiological Exposure Devices (RED) planted on a university campus	20 adult and 20 pediatric patients with detailed patient profiles and required medical evaluation
2016 Primarily Webinar	1 kiloton improvised nuclear device (IND) detonated in a metropolitan area 500 miles away	30 patients (adult or pediatric depending on the hospitals focus) with special emphasis on Family Information Centers to connect patients with their families
2017 Primarily Webinar	1 kiloton improvised nuclear device (IND) detonated in a metropolitan area 500 miles away	Triage of three complex patients (adult and pediatric patients were provided for the different treatment facilities) with various comorbidities and

		a limited number of beds available requiring the decision of which one patient to admit

RITN Sponsored Regional Tabletop Exercises:

During 2017 seven regional tabletop exercises were conducted across the nation. Regional tabletop exercises were developed by RITN to fill a gap in planning efforts. Communities prepare for disasters that effect their community or their region; but few had considered the surge of casualties from a distant radiological incident. We brought together leaders in public health, emergency management, law enforcement, healthcare, federal agencies and non-governmental agencies that support disaster response. Then we presented a scenario where a radiological disaster occurred more than 1,000 miles away (e.g. for Chicago's exercise the disaster was in New York); and asked how they would prepare to receive a surge of medical casualties in 7-10 days (per the RITN concept of operations).

RITN Sponsored Full-Scale and Functional Exercises:

During 2017 one full scale exercise was sponsored by RITN; this was held at Spectrum Health, Grand Rapids, Michigan. Each year RITN solicits hospitals from RITN to submit proposals to conduct full-scale or functional exercises. A full scale exercise is significantly larger in scope than a functional exercise. Functional exercises test one specific area such as public communications, emergency operations center activation or patient tracking. Full scale exercises include all aspects of the response. Those given awards receive funding to help conduct the exercise; in exchange for the funding RITN receives copies of all exercise planning and execution materials which are posted online to help other organizations plan for and conduct their own radiological disaster exercises. For the Spectrum Health exercise seven critical improvement items were documented to be corrected to improve preparedness; ranging from improving patient flow, the triage process, delegation of authority, and coordination with the healthcare coalition.

The hospitals which conducted an exercise with RITN funding under this grant are listed in Table 2 below:

Table 2. 2017 RITN Funded Exercises by Hospital and Exercise Type.

Hospital	Exercise Type
Spectrum Health	Full Scale Exercise

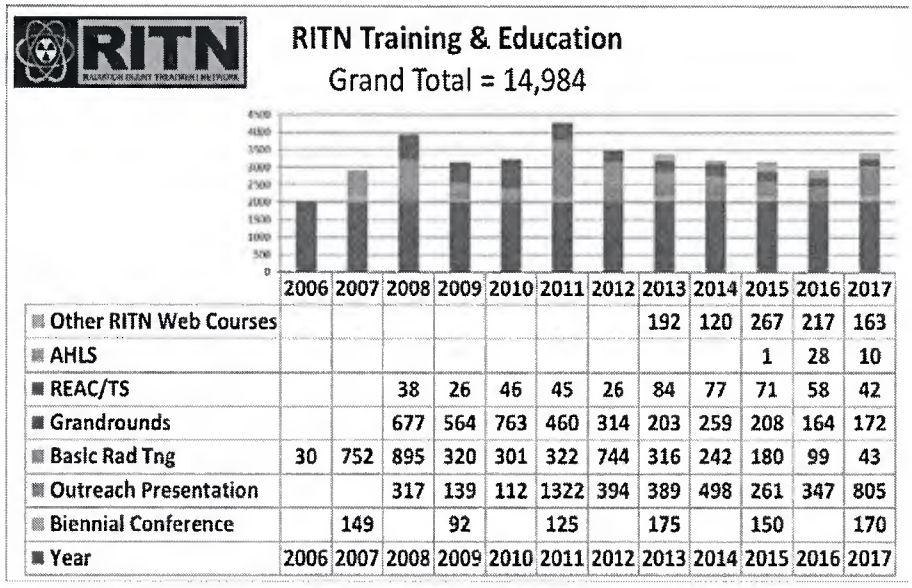
Rush University Hospital	Functional Exercise
Massachusetts General Hospital	Functional Exercise
Children's Hospital of Philadelphia	Regional Table Top Exercise (TTX)
Children's Mercy Hospital	Regional TTX
Texas Children's Hospital	Regional TTX
Wake Forest Baptist Health	Regional TTX
University of Arizona Medical Center	Regional TTX
Spectrum Health	Regional TTX
Memorial Sloan Kettering	Regional TTX

Training tasks:

RITN centers are asked to conduct training with the intent to educate and increase the awareness of RITN and its efforts to the appropriate response community. Training options continue to be publicly accessible online at no cost to anyone who is interested. In addition, the in person training option has expanded to include an Advanced HAZMAT Life Support (AHLS) for Radiological Incidents course. As shown in Figure 6 the training options continue to grow, centers can now choose between conducting Basic Radiation Training, having a physician or Advanced Practitioner complete the REAC/TS training, hosting an AHLS course, conducting an Acute Radiation Syndrome Medical Grand rounds session, and having a site assessment conducted. In addition, centers can conduct community outreach and education using the RITN Overview Presentation. All of these materials, with the exception of the REAC/TS training, are available unrestricted, through the RITN website. The RITN web based training catalog includes:

1. Introduction to RITN
2. RITN Concept of Operations
3. GETS 101
4. Satellite telephone 101
5. Basic Radiation Training
6. Non-medical Radiation Awareness Training
7. Radiation Safety Communication Course

The online learning management system allows RITN center staff to complete the full course at their own pace and receive an electronic certificate of completion after meeting all the course objectives and knowledge assessments. Since 2006, RITN has had a hand in the disaster response training or education of approximately 15,000 medical personnel and staff affiliated with RITN hospitals (Figure 7).



	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017
Other RITN Web Courses								192	120	267	217	163
AHLS										1	28	10
REAC/TS			38	26	46	45	26	84	77	71	58	42
Grandrounds			677	564	763	460	314	203	259	208	164	172
Basic Rad Tng	30	752	895	320	301	322	744	316	242	180	99	43
Outreach Presentation			317	139	112	1322	394	389	498	261	347	805
Biennial Conference		149		92		125		175		150		170
Year	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017

Figure 7. RITN center staff training accomplished by year.

In 2011, RITN initiated the Site Assessment program which has conducted 48 assessments of RITN hospitals (Figure 8). RITN Control Cell staff members review existing documentation at RITN transplant centers using a standardized checklist (Figure 8) to assess overall preparedness. Areas evaluated include Casualty Processing, Outpatient Treatment of Casualties, Inpatient Treatment of Casualties, Coordination with City, State and Regional Assets, and Documentation.

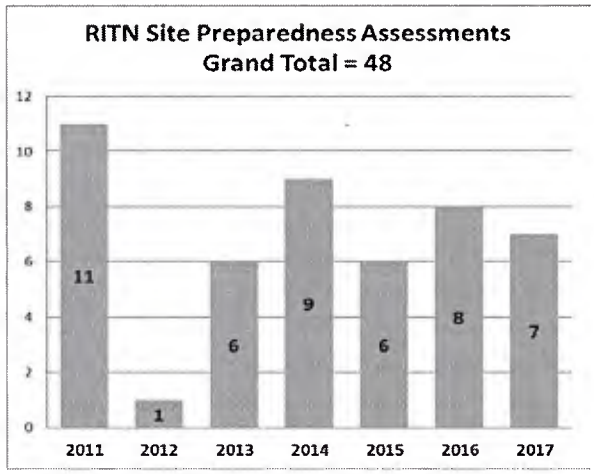


Figure 8. RITN center site assessments by year.

The Site Assessment Checklist formed the basis for revisions to the standard operating procedure (SOP) template that all centers used to update their local SOPs.

The RITN continuously seeks to formalize and develop further partnerships with federal agencies and organizations.

Memoranda of Understanding (MOU) have been established with the following groups to collaborate on preparedness efforts:

- ASBMT since 2006
- Department of Health and Human Services – Office of the Assistant Secretary for Preparedness and Response (HHS-ASPR) since 2007
- AABB-Disasters Task Force since 2008
- European Group for Blood and Marrow Transplantation - Nuclear Accident Committee (EBMT-NAC) since 2011

Additionally, the RITN maintains informal relationships to increase awareness about RITN worldwide through close interaction with:

- Biomedical Advanced Research and Development Authority (BARDA)
- Health Resources and Services Administration (HRSA)
- World Health Organization - Radiation Emergency Medical Preparedness and Assistance Network (WHO-REMPAN)

- Radiation Emergency Assistance Center and Training Site (REAC/TS)
- Armed Forces Radiobiology Research Institute (AFRRI)
- National Institute of Allergy and Infectious Diseases (NIAID)
- National Institutes of Health (NIH) - National Library of Medicine (NLM) - Radiation Emergency Medical Management (REMM)
- American Hospital Association (AHA)
- Association of State and Territorial Health Officials (ASTHO)
- National Association of City and County Health Officials (NACCHO)
- Veteran's Administration Health System
- Centers for Medical Countermeasures Against Radiation (CMCR)
- National Alliance for Radiation Readiness (NARR)

RITN uses Health Care Standard® (HCS®) software to consolidate participating hospitals Capability Reports and to communicate situation status updates to the network through a web based interface. Annual tests are conducted to ensure that users are familiar with the system and that it is capable of receiving and consolidating submitted data. This system allowed RITN to collect the bed availability and on-hand G-CSF quantities throughout the network during a prior grant period.

The Assistant Secretary for Preparedness and Response from the Department of Health and Human Services has been a partner since the foundation of RITN. This partnership is formalized through an MOU and is prominently displayed on the Department of Health and Human Services website for Public Health Emergencies on the Chemical, Biological, Radiological, Nuclear and Explosive Branch page, (http://www.PHE.gov/about/oem/cbrne, and Figure 9):

Figure 9. Chemical, Biological, Radiological, Nuclear and Explosive Branch webpage noting the partnership with RITN.

NMDP's critical functions must remain operational during contingency situations that directly affect the Coordinating Center.

Operational Continuity Planning (OCP) is essential for world-class organizations to meet the myriad of 21st century emergencies; this is evident by the visibility of many standards, such as ISO 22301:2012 which specifies requirements to plan, establish, implement, operate, monitor, review, maintain and continually improve a documented management system to protect against, reduce the likelihood of occurrence, prepare for, respond to, and recover from disruptive incidents when they arise. The OCP is comprised of plans, systems, and processes for resuming NMDP operations in the shortest time possible following a severe operational disruption. OCP focuses on increasing the resiliency of the staff essential to conduct recovery operations, the facilities required to house these staff members, and the specialized long lead time equipment needed to connect these staff members to our data center from remote locations.

The OCP mitigates the effect of the many incident categories that may adversely impact NMDP operations. The OCP does not specifically plan for each possible hazard to the organization, rather it has a broad scope with a flexible and scalable response to allow for a successful activation in response to various catastrophic events ranging from fires, flooding, pandemics, extended evacuations (due to building damage, local chemical spill, or other hazards making the facilities unusable), to extended service outages such as water, electricity or sewer services. The OCP does not include NMDP Data Center incidents, as these are covered by the Information Services department through the Disaster Recovery program. NMDP continues to annually test its OCP to validate functionality with the continually changing information system environment as well as the growing organization structure and operational complexity.

The NMDP requires specialized technical staff to accomplish the organization's mission. The technical skill sets required are not readily replaceable. Without these staff members, the NMDP would not be able to support its network of centers in their daily operations and research programs. The NMDP OCP outlines procedures to allow resumption of operations within 72 hours of a catastrophic disruption. This is essential for the HCT community that relies on NMDP staff and systems for timely access to critical graft sources.

During the grant period, the NMDP updated the Operational Resiliency Plan (ORP) and all supporting documentation. The Operational Resiliency Steering Committee reviewed changes and additions to the plan at the annual meeting. The committee is chaired by the Chief Medical Officer and seated by the Chief Information Officer; Chief Financial Officer; Chief Legal Officer; Chief Operating Officer; and Chief Human Resources Officer.

Development of Science and Technology for Rapid Identification of Matched Donors

Increasing the resolution and quality of the HLA testing of volunteers on the Registry will speed donor selection.

Increased diversity of newly recruited donors

In NMDP FY17 (Oct. 2016-Sept. 2017), NMDP donor centers (including Department of Defense (DoD)) and recruitment groups recruited 147,608 minority race and 189,873 White donors, for a total of 337,481 U.S. donors added to the registry. Navy funding supported the HLA typing of 175,131 donors (excluding DoD) of this culturally diverse group (44% minority).

Advancing technology improved performance and pricing

The NMDP typing strategy maximizes the use of funds by utilizing new typing methodologies that deliver a higher resolution of results at a lower cost than previous methods. The overall goal

is to ensure that new donors are listed on the registry with the best possible resolution and number of loci tested. This is particularly critical during times of a contingency where well HLA-characterized adult donors must be readily matched to patients in need of HCT for ARS. Since January 2017, 100% of newly recruited donors are typed with this methodology at HLA-A, B, C, DRB1, DQB1, DPB1, exon-based for DRB3/4/5, ABO/RhD, and the CCR5 delta 32 mutation.

Enhancing Non-HLA data for selected donors

Transplant centers utilize donor CMV status and blood type (ABO/Rh) as non-HLA selection factors when multiple equally well-matched donors are available. Historically, the only process to obtain this information was to request the potential donor on behalf of the patient, obtain a fresh blood sample, and perform IDM tests that include the donor blood type and presence/absence of circulating antibodies to CMV. CMV antibodies are present in oral transudate fluid, in addition to blood serum. Over the course of several experiments, two different NMDP contract laboratories have been able to satisfactorily use a modified assay to test for the CMV virus when flocked swabs were used to collect oral specimens. The studies achieved both 100% positive predictive values and assay specificity, as well as >85% assay sensitivity and negative predictive values, when a small percent (<9%) of results were excluded as equivocal. Incorporation of this testing, in parallel with the HLA testing, of registry members at the time of recruitment, would provide a presumptive CMV serostatus to enhance the non-HLA information available and aid the transplant center with quicker optimal donor selection. An assessment of the value of presumptive CMV testing will be conducted in the next grant period.

ABO/Rh and CCR5Δ32 mutation at Recruitment by DNA-based testing

As of October 01, 2014, all recruitment samples receive DNA based ABO/RhD testing along with HLA testing as noted above. As of October 2016, all recruitment samples receive DNA based testing to detect the presence/absence of CCR5Δ32 mutation.

Donors homozygous for the CCR5Δ32 deletion are of interest in HCT for patients infected by both HIV-1 and a hematologic malignancy. The mutation confers natural HIV resistance to individuals carrying two copies (homozygotes), while heterozygous individuals show increased resistance and lower viral loads compared to wild type. The addition of this testing to the donor recruitment panel will allow NMDP to characterize the CCR5Δ32 deletion frequency in the diverse unrelated donor populations listed on the registry. This analysis will be completed in the next grant period.

Quality of HLA typings improved

The NMDP's comprehensive quality control (QC) program has supported the successful increase in the quality of HLA typing received through the contract laboratory network. Blind QC samples are added to each weekly shipment of new donor recruitment samples. These QC samples comprise 2.5% of each shipment and are indistinguishable from the other samples. There are more than 1,000 QC Masters in active rotation, representing over 87% of common HLA alleles and 13% of well-documented HLA alleles. In order to maintain a robust and diverse inventory of QC Master samples into the long term future, a program to obtain samples from registry donors with desirable HLA types and other unique immunogenetic factors has been developed and implemented. A software application has been developed and released in the past year for business users to manage QC sample inventory and track incoming test results. This will allow staff to track sample age, document sample lineage, and detect patterns in reporting errors in real time.

Proactive Information Session, Phase 2

During the grant period, the Immunogenetic Operations and Research group completed analysis of the Proactive Information Session Project-Phase 2, in which male donors under 25 years old with common HLA typing and thus in high demand for searching patients were prospectively contacted and their registry information upgraded with additional HLA typing, blood type, and CMV status. Killer Immunoglobulin-like Receptor (KIR) typing results were also available for these donors upon request by the transplant center. These high demand donors were also given a proactive information session about the donation process.

After 1 year of enrollment, 61 donors had fully completed the proactive session process. Incoming patient searches were monitored daily for 1 year and U.S. transplant center searches that had not yet placed an order (i.e. preliminary) and who had a workup ready donor as a potential match were enrolled in the study. Overall, 39 patients were enrolled in this study and 48 total donor recommendations were made for these patients. Recommendations were given to the transplant center (TC) by the NMDP case manager. They alerted the TC that the donor had received an information session, and was prepared to go directly to work up, if necessary.

A total of 26 of the 61 donors in the workup ready donor pool were activated by a TC for a U.S. patient, 9 of those from the recommendation of NMDP and an additional 17 that were independently selected by the TC. Of these 26 activated donors, only 2 were requested directly to go to workup (WU) by the TC. Thus, even when provided with a fully matched WU ready donor, many transplant centers prefer to perform their own confirmatory typing before selecting a donor for WU.

A comparison was made looking at the donors activated that were WU ready versus donors activated outside of the WU ready pool. Overall, the WU ready donors had a 54% availability rate and took on average 24 days to go through the formal to workup process. Donors selected outside the WU ready pool had an availability rate of 62% and took on average 41 days to complete the formal to workup process.

In summary, this project showed high utilization of donors from this study, nearing 50%, both by active recommendation from the NMDP and via passive selection utilizing donors that completed the Proactive Information Session process and had increased data available (e.g. HLA, CMV, ABO). Unfortunately, the availability rate of these donors was no higher than baseline donor availability. However the donors who were available proceeded to workup faster than non-project donors. One of the main goals of the study was to encourage TCs to move directly to workup with these project donors. This only occurred two times suggesting that a change in practice may be required at the TC side to support this new process.

Primary DNA typing data can be used within the registry to improve the quality and resolution of volunteer donor HLA assignments.

An HLA assignment obtained by SSOP, DNA-based testing methods is derived from the positive and negative hybridizations of oligonucleotide reagents that define the presence of specific nucleotide sequences. Using this information and a list of known HLA alleles with their primary sequences, the typing laboratory interprets the hybridization results into possible allele combinations (interpreted data). The information for which polymorphic nucleotide sequences are present or absent is termed "primary data." Similar primary data are available from other DNA-based methods, sequence specific primers (SSP) and sequence-based typing (SBT).

Data Standards Hackathon

Following three successful Data Standards Hackathons (DaSH) in DC, California and Minneapolis during a prior grant period, four Hackathon events were organized in the past year.

DaSH 4, Vienna, November 2016

This meeting was co-hosted by Gottfried Fischer, the previous president of European Federation for Immunogenetics, and took place at the University of Vienna. Forty coders and scientists attended, including 17 people from Europe.

DaSH 5, Berkeley, CA, March 2017

This meeting was co-hosted by Jill Hollenbach (UCSF) and Steve Mack (CHORI). 35 coders and scientists attended.

DaSH 6, Heidelberg, Germany, May 2017

This meeting was co-hosted by Hans-Peter Eberhard (ZKRD). 24 coders and scientists including 13 people from Europe.

DaSH 7, Utrecht, Netherlands, Nov 2017

This meeting was hosted by GenDx and 39 attendees from industry, academia and donor registries. The meeting focused on a number of topics:

1. Modeling peptide processing and presentation pathways (NetChop/Chipper, NetMHC), NeoAntigen Prediction, Whole Genome Sequence Analysis
2. HL7-FHIR: Tools for conversion of HML to FHIR bundles, FHIR Clinical Genomics, & Sync for Genes
3. Tools to support analysis of whole gene sequencing of HLA and KIR. These include Gene Feature Enumeration (GFE), Feature Service and the Allele Calling Tool (ACT).
4. Analysis of Primate MHC data using 17th IHIWS Informatics tools
5. Haplotype Frequency Curation. This is a new web service being develop to make haplotype frequency data from global populations available programmatically to software that consumes this frequency data (e.g. to make matching predictions).

There have been over 100 DaSH participants so far from CHORI, UCSF, Stanford and UC Berkeley, UCLA, the National Marrow Donor Program (NMDP) in Minneapolis, Children's Hospital of Philadelphia (CHOP), and the Department of Defense Marrow Program; the German Marrow Donor Program (ZKRD), the Center for International Blood and Marrow Transplant Research (CIBMTR), the Anthony Nolan Bone Marrow Trust (UK), the University of Vienna, and Maastricht University. Corporate participants include NGS platform vendors Illumina (San Diego), Pacific Biosciences (Mountain View) and Roche Molecular Solutions (Pleasanton); NGS software vendors Omixon (Prague), GenDx (Leiden), Immucor (Norcross, GA), ThermoFisher (Waltham, MA), and CareDx (Brisbane); and bioinformatics developers Knowledge Synthesis (Berkeley).

The work has focused on two main areas.

- Data standards for HLA: specifying principles for annotation and testing out data formats, tools and service with producers and consumers working together to provide rapid assessment. The goal is to develop a public "ecosystem" which is a set of tools and standards

to create a shared facility for the storage, exchange and analysis of HLA and KIR data, project related data, and analytic results building on Minimal Information for Reporting Immunogenomic NGS Genotyping (MIRING), Histoimmunogenetics Mark-up Language (HML) and GL-service.

- HL7 FHIR (Fast Healthcare Interoperability Resources): exploring the use of HL7 as a convenient platform for exchanging HLA typing data, particularly by providing the code to test messages, as well as trouble shooting any problems in the data message exchange. This also included work on CCR5 and ABO/Rh reporting, and preparing a new HML schema to support nested specifications like FHIR.

HML FHIR Converter

We developed a web server for converting HML messages into bundles of HL7-FHIR resources in order to demonstrate the conformance of HL7-FHIR clinical genomics resources with the complex MIRING principals and HML schema. This system is based on the HLA reporting bundle strategy in the FHIR genomics implementation guidance document. Resources used included Sequence, Specimen, Organization, Patient, Bundle, and the clinical genomics profiles (Observation, DiagnosticReport, DiagnosticRequest, HLA Genotyping Results).

Our software is available publically with separate server and client repositories.

We are continuing to validate this approach with HLA typing vendors at the Data Standards Hackathon (DaSH) events. As part of the Nov 2017 DaSH event, commercial partners (CareDx, GenDx, Omixon) started to test uploading HLA typing reports to a FHIR server hosted by NMDP. We continue to promote this approach with HLA typing and integration software vendors because it will facilitate better integration with Electronic Medical Records (EMR) software and allow HLA sequence information to be brought closer to the physician for more informed decision making.

HL7 (Health Level 7) Genomics

New and emerging technologies force the development of new and emerging standards. For example, the immunogenomics NGS community has recently developed a set of principles describing MIRING. However, these guidelines are not implementable using currently available data standard formats. The approach has been to go forward in developing a technical implementation of the MIRING guidelines by extending HML, and at the same time work with the larger genomics community standards being developed (Global Alliance for Genomics and Health, ClinGen) and healthcare interoperability standards communities

HL7. By working with these communities, the development of new standards informed by MIRING principles and HML 1.0 specifications has been enabled. While HML 1.0 meets the current needs for reporting NGS based genotyping, it is not yet poised to interoperate seamlessly with clinical electronic medical record systems (EMRs). It is proposed to evolve HML so that the next major version (HML 2.0) will be based on HL7 FHIR and should more easily integrate with EMRs.

The primary activity towards this goal in the past year has been:

- Continued development of HL7 FHIR Profiles for HLA and KIR reporting through participation in the HL7 Clinical Genomics (CG) Work Group.
- Development of an HLA Terminology Service
    - A proof-of-concept HL7 FHIR terminology service has been developed [http://mac-and-fhir-prototype.us-east-1.elasticbeanstalk.com/doc/]
    - A static FHIR Bundle containing CodeSystem and ValueSet FHIR resources for HLA nomenclature has been made available [https://s3.amazonaws.com/nmdp-fhir-terminology/who/fhir-imgt-hla-terminology-20170729.zip]
- Development of an open-source HML to FHIR converter application
  A series of libraries has been developed and made available for this effort

    - https://github.com/nmdp-bioinformatics/hml-to-fhir
    - https://github.com/nmdp-bioinformatics/service-hml-fhir-converter
    - https://github.com/nmdp-bioinformatics/hml-fhir-mongo
    - https://github.com/nmdp-bioinformatics/service-hml-fhir-converter-api
    - https://github.com/nmdp-bioinformatics/service-hml-fhir-converter-models
- Working with vendors to include HML 1.0 and newly developed HL7 FHIR resources into their products
    - **EPIC** –An EPIC App Orchard application for patient submission to CIBMTR has been developed (described in more detail in section IID.1.1).
    - **CareDx** – Representatives have joined the HL7 Clinical Genomics Work Group and are collaborating on the development of FHIR resources and profiles for reporting HLA.
    - **LabCorp** is committed to a pilot project to submit HL7-FHIR HLA typing reports.
    - **Blood Centers of Wisconsin** has drafted a pilot for sending full-HLA sequence data from the laboratory to their transplant centers for nomenclature-agnostic matching.
    - **Stanford** has agreed to participate in a pilot where they will work with their lab

software vendor (**M'Tilda**) to testing submission of HLA lab reports using HL7-FHIR.

- Informing the larger genomics communities of the unique needs of HLA and KIR This includes participation with the data modeling efforts of Global Alliance for Genomics and Health, and the ClinGen Allele Data Model.
  - We have continued participating in the HL7-FHIR Clinical Genomics Work Group, and have sent several participants to FHIR connectathons participating in the Clinical Genomics track.
  - Six people attended FHIR Dev Days in Nov 2017.
  - A new FHIR resource called BiologicallyDerivedProduct to describe transplant material (stem cells, organs, blood, etc) was proposed, which is now in the current build of FHIR and is in the R4 ballot. (http://hl7.org/fhir/2018May/biologicallyderivedproduct.html)
  - A public development FHIR server using HAPI java libraries (hapifhir.io) was deployed. This is found on http://fhirtest.b12x.org/.
  - A 1-day symposium on HL7-FHIR followed by a 2-day hackathon in Minneapolis on July 25-27 was organized.

Registry data on HLA allele and haplotype frequencies and on the nuances of HLA typing can be used to design computer algorithms to predict the best matched donor or cord blood unit.

HLA allele and haplotype frequencies are central to matching and the selection process as well as for more strategic tasks such as modeling registry growth or estimating match rates beyond the typing resolution of the donors in the registry.

Global HapLogic

We have developed a prototype implementation of HapLogic^{SM} that applies global population frequencies developed under previous years of this grant to assigning match predictions to all donors and CBUs in the Bone Marrow Donors Worldwide (BMDW) database for display in the upfront search of Be The Match. This system is undergoing validation and haplotype frequency development.

Modeling Coverage Gaps in Haplotype Frequencies

We developed a method for addressing the problem that, due to the heavy-tailed frequency distribution of HLA haplotypes, computational methods that use this data often have to deal with

rare haplotypes that have not been observed in the reference frequencies. Matching algorithms like HapLogic, for instance, face this situation on as many as 25% of the donors. Current methods for addressing this situation are crude – resorting to individual allele frequencies to make predictions. We developed a Baysian inference method for extending haplotype frequency distributions using a model where new haplotypes are created by recombination of observed sub-haplotypes. This method preserves linkage disequilibrium information in smaller haplotype components and has been shown to provide improved prediction over previous methods. The method has been published a paper titled: "Modeling coverage gaps in haplotype frequencies via Bayesian inference to improve stem cell donor selection".

Multi-race Bayes

We have further developed and validated a method for imputing HLA using a Bayesian framework where the a subject's HLA was imputed and the most probable continental origin (Africa, Asia, etc.) was assigned to the subject's haplotypes. This method was applied to a cohort of 110,000 donors who participated in study that collected geographical ancestry information by questionnaire and compared the results to the HLA and the self-identified race. The results are being prepared for publication but the main finding is that the combination of self-identified race and geographical ancestry combined provide more information and correlate better with HLA genetics than either variable on its own.

Reducing the time and effort required to identify closely matched donors for patients in urgent need of HSC transplants will improve access to transplantation and patient survival in the context of a contingency response and routine patient care.

Donor Match Rate Studies

Temporarily Unavailable Donor Contact Project

In this project, donors with a TU status (temporarily unavailable) with an available date (i.e. data at which transplant centers (TCs) can request donor for activity) in the following month who are best/only for a searching patient are identified. The donor is contacted and provided with detailed messaging about their importance to the patient. At that time, their willingness to proceed once their TU date expires is assessed. If they are not interested in proceeding they are deleted from the registry and this information is provided to the transplant center in the event they were waiting for this donor prior to pursuing other therapeutic options. If the donor commits to being available once their TU date expires they are given a health history questionnaire and given further information on the process, as needed. This information is also communicated to the transplant center.

This project began in March, 2017. Table 3 shows the number of donors and availability rate of after contact to confirm they are able at the end of the TU period. Since March, 107 donors have

been contacted with 30 (28%) available when their TU date expired, to date. Twelve of these available donors have been requested for the patient. One donor went on to donate stem cells for a patient and a second donor is scheduled for donation at the end of December.

Table 3. TU Donor contact project results

Donors contacted	107
Donors available	30
TU date extended	20
Deleted	28
Duplicate donor	1
Donors contacted	41
Donors available	11
TU date extended	4
Deleted	17
Pending	8
Duplicate donor	1

Selection, Typing and Transplant (STaT)

Patients transplanted earlier in their disease cycle are associated with better outcomes and better chance at survival. The median time from preliminary search to donor workup is over 100 days, potentially putting patients at higher risk for relapse and disease progression in addition to additional cost and morbidity due to the additional need for immune therapy (chemotherapy and/or radiation). Haploidentical transplant numbers continue to increase, potentially as a result of the perceived increased time and cost associated with unrelated donor transplant. Transplant centers may be using less desirable haploidentical donor (per treatment protocols) because of slow delivery of unrelated donors.

The STaT study is aimed to determine the feasibility of identifying a suitably matched unrelated donor in an expedited timeframe (14 days). The goal is to decrease the overall timeline to transplant for urgent patient cases and allow clinical decisions to be made with the full complement of stem cell product choices available for best treatment of the patient.

The study has enrolled patients from 2 different transplant centers and currently ready to add 2 more transplant centers. The study has enrolled 43 patients and 9 collections completed (7 more scheduled) with the median day from selection to transplant 68 days. NMDP delivered a WU ready donor in 14 days or less nearly 90% of the time. The majority of the patients not meeting the 4-6 week transplant target were delayed due to a patient related issues.

NIH Search Support

The National Institutes of Health (NIH) has been accepted as an NMDP transplant center since 2007. Prior to that time, the NIH, representing our nation's premier medical research endeavor, was not applying their considerable problem-solving skills to issues surrounding unrelated donor transplantation. The NMDP, with ONR support, set out to remedy that deficiency by entering into collaboration with NIH. This collaboration has been extremely successful.

The NMDP is collaborating with intramural NIH transplant programs from the National Cancer Institute, the National Heart Lung and Blood Institute and the National Institute of Allergy and Infectious Diseases. These programs are investigating alternative approaches in unrelated donor transplantation to improve patient outcomes. The actual transplants and the investigational portions of each transplant (i.e., the research protocols) are supported entirely with NIH funds. Navy funding supplies support for donor identification, selection and collection. NMDP donors are not research subjects on these protocols because the donors are making standard donations for accepted transplant indications. The research component of these transplants is conducted entirely by NIH intramural program staff and funded entirely with NIH dollars. The NMDP provided support for the collection of 13 products (4 PBSC, 2 CBU, 5 marrow and 2 therapeutic T cell) under the current grant.

Rapid identification of potential donors for newly diagnosed AML patients

The Southwest Oncology Group (SWOG) has identified the time from diagnosis of Acute Myelogenous Leukemia (AML) to transplant as critical for successful treatment of patients with cytogenetically defined high risk disease. Proceeding to transplant within four months of diagnosis for patients with high risk disease in first chronic remission could potentially improve the overall disease free survival rates. Currently, these patients are referred for transplant following cytogenetic screening and several lines of therapy. The initial diagnosis and treatment phase can take several months significantly delaying the initiation of an unrelated donor search and making transplant within four months highly unlikely. NMDP/CIBMTR up front involvement would permit the rapid identification and pre-search screening of potential donors, so patients will be well along in the search process when/if ultimately referred for HCT.

In April 2013 SWOG initiated the clinical trial entitled, *"S1203: A Randomized Phase III Study of Standard Cytarabine plus Daunorubicin (7+3) Therapy or Idarubicin with High Dose Cytarabine (IA) versus IA with Vorinostat (IA+V) in Younger Patients with Previously Untreated*

Acute Myeloid Leukemia (AML)". The trial was a randomized phase III trial of cytarabine and daunorubicin hydrochloride or idarubicin and cytarabine with or without vorinostat to see how well they work in treating younger patients (18-60 years old) with previously untreated acute myeloid leukemia. Drugs used in chemotherapy, such as cytarabine, daunorubicin hydrochloride, idarubicin, and vorinostat, work in different ways to stop the growth of cancer cells, either by killing the cells or stopping them from dividing. Giving more than one drug (combination chemotherapy) and giving the drugs in different doses and in different combinations may kill more cancer cells. It is not yet known which combination chemotherapy is more effective in treating acute myeloid leukemia. The study included a transplant arm for patients diagnosed with high risk cytogenetics following the initiation of induction therapy (see Figure 10 below). NMDP/CIBMTR supported the project using ONR grant funds to provide study-specific sample collection kits for all enrolled patients, processed samples, typed, HLA typing patients that were diagnosed as cytogenetic high-risk and generated preliminary search strategy reports to assist in the identification of donors and/or CBUs through the NMDP. The resulting search information was provided to the S1203 transplant arm principal investigator who shared the data with the referring physician.

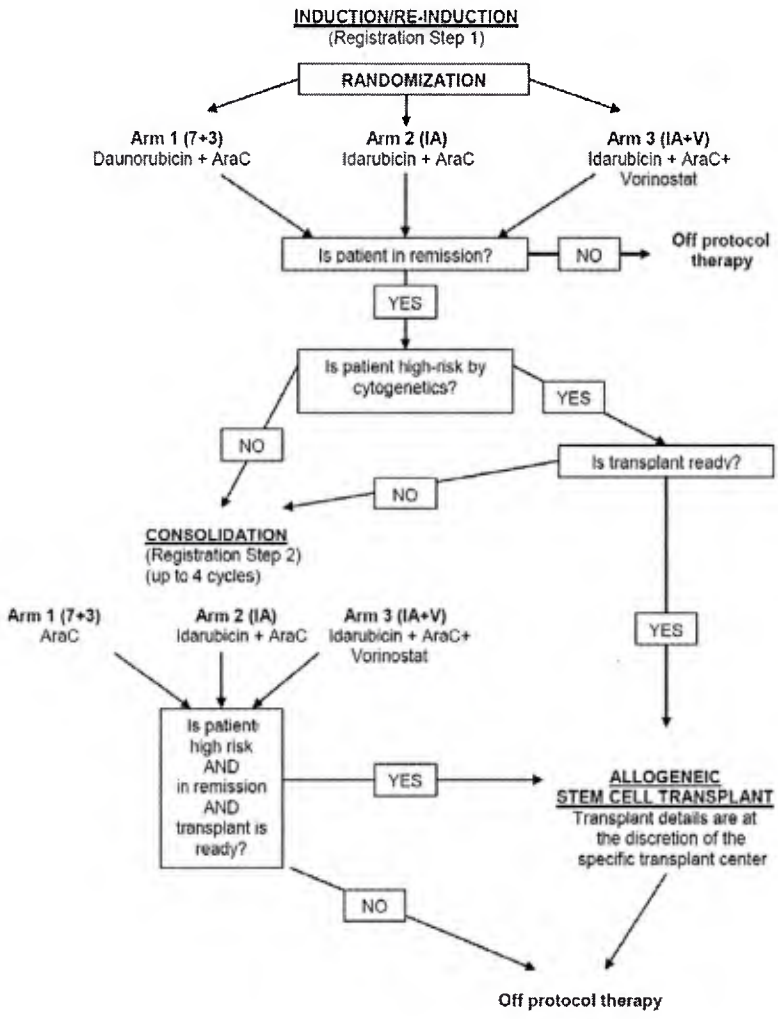


Figure 10. S1203 trial randomization and treatment schema.

The study opened in April 2013 and accrual was completed November 2015. The results of the transplant cohort were reported as an oral abstract at the 2016 ASH annual meeting. Of 738 eligible patients (median age, 49 years; range, 18-60), 159 (22%) had high-risk cytogenetics, of whom 60 (38%), 61 (38%), and 38 (24%) received induction with 7+3, IA, or IA+V, respectively. A total of 107 of the 159 high-risk patients achieved complete remission (CR1) (67%). HCT was performed in 317 of all 738 patients (43%) and 68 (64%) of the high-risk patients received a transplant in CR1 ($p<0.001$ compared to historical rate of 40%). Twenty-five

(37%) had a matched related donor, 31 (45%) had a matched unrelated donor, 3 (4%) had a mismatched related donor, 8 (12%) had a mismatched unrelated donor, and 1 (1%) received an umbilical cord blood transplant. Median time to HCT from CR1 was 76 days (range, 20-365). Fifty-seven patients (86%) received a myeloablative regimen and 9 (14%) reduced-intensity conditioning. Reasons for 39 high-risk CR1 patients not receiving a transplant in CR1 were: co-morbidities (n=1), death (n=6), no insurance (n=1), no donor (n=1), physician decision (n=3), patient decision (n=3), relapse (n=6), other (n=10), or unknown (n=8). The 2-year relapse-free (RFS) estimate in the entire high-risk cohort is 32%, significantly higher than the 22% historical rate (p=0.05). Median RFS in the high-risk CR1 cohort (n=107) was 10 months [range, 1-32* (censored) months]. RFS and overall survival (OS) were similar among HCT patients using matched related [1 year estimates: 40% (95% confidence interval (CI) 27%, 74%) and 56% (37%, 74%), respectively] and matched unrelated [1 year estimates: 52% (37%, 75%) and 56% (37%, 74%), respectively] donors in CR1. The HR (reference = unrelated) for RFS was 0.67 (0.32, 1.37) and for OS was 0.88 (0.41, 1.90). Median overall survival (OS) among all patients in the high-risk cohort (n=159) was 12 months [range, 1-33* (censored) months] and was 18 months [range 3-33* (censored) months] for those transplanted in CR1 (Figure 11). The study clearly demonstrated that in newly diagnosed adults with AML age 18-60, early cytogenetic testing with an organized effort to identify a suitable allogeneic HCT donor led to a CR1 transplant rate of 64% in the high-risk group, which in turn led to a significant improvement in RFS over historical controls. Better outcomes in poor prognosis AML patients may be achieved simply by rapidly finding unrelated donors and performing allogeneic HCT in CR1 as soon as possible. The manuscript is currently under review in the New England Journal of Medicine.

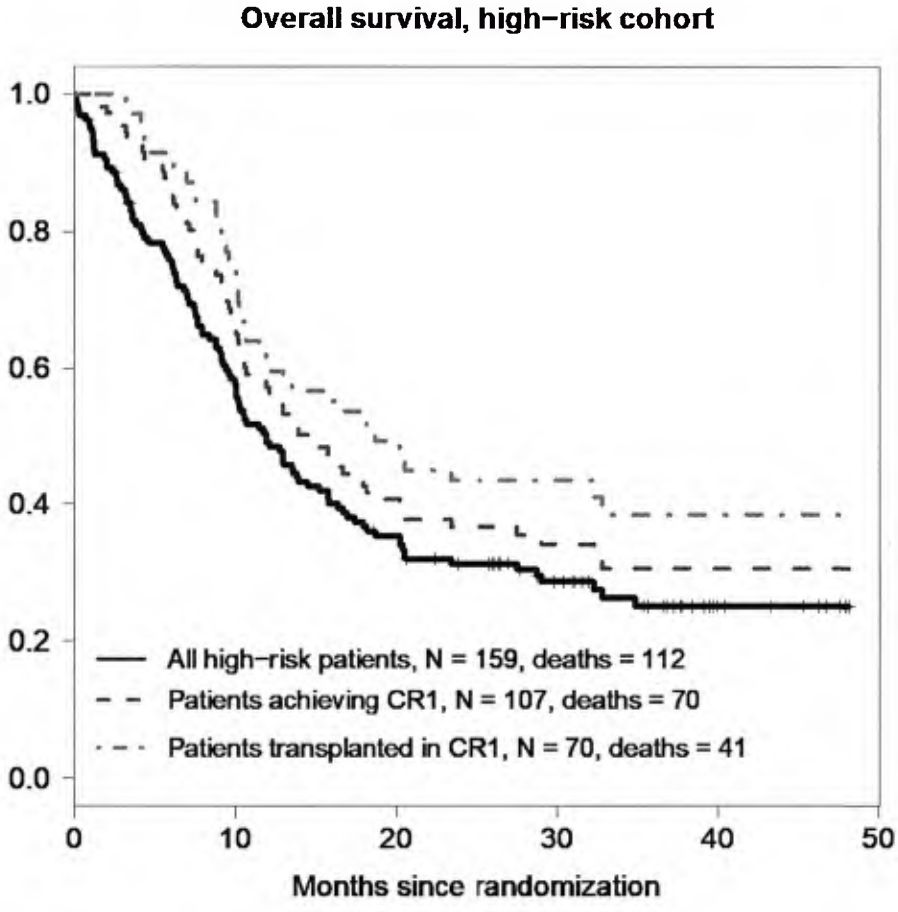


Figure 11. Overall survival of high risk cytogenetic AML patients enrolled in SWOG 1203.

Immunogenetic Studies in Transplantation

IIC.1 Objective 1

HLA mismatches may differ in their impact on transplant outcome, therefore, it is important to identify and quantify the influence of specific HLA mismatches. In contingency situations, it will not be possible to delay transplant until a perfectly matched donor can be found.

Donor/Recipient Pair Project

A retrospective Donor/Recipient Pair HLA typing project to characterize class I (HLA-A, B and C) and class II (HLA-DRB, DQB1, DQA1, DPA1 and DPB1) alleles of stored donor/recipient paired samples was initiated in 1994. To date, over 29,000 unrelated paired samples and more than 1,900 related paired samples from the CIBMTR research repository have been fully

characterized and the resultant data are available for research use. The data are stored in an NMDP developed database and is available to any researcher with a CIBMTR-approved study wishing to analyze the impact of matching as either the focus of, or as a variable, in a research study. To date, 177 published research studies (not including abstracts) have used these data, including the seminal publication from Lee et al (Blood 2007), describing the importance of high resolution HLA matching in unrelated donor transplantation that formed the basis for NMDP's updated guidelines for unrelated adult donor HCT HLA matching (Spellman et al Blood 2012).

The typing strategy for the donor/cord and recipient samples changed in 2016 to take advantage of the high quality and low cost typing available through the registry typing laboratories. All samples are tested for whole gene at HLA-A, B and C, extended gene at DRB1, DQB1, and DPB1 and presence/absence for the 16 KIR loci. During the last grant period, HLA and KIR typing was completed on 2,720 unrelated and 1,000 related adult donor transplant pairs for the project. After successful completion of the typing, each pair was audited for use in analyses. All samples are selected in collaboration with the CIBMTR statistical center to ensure the additional cases would benefit ongoing and future analyses. Transplantation practices are constantly evolving and the project will continue to enroll the most recent transplant pairs to ensure that changes in practice can be evaluated with fully quality controlled high resolution HLA data.

Full HLA Gene Typing Match Assessment

The impact of amino acid differences outside of the antigen recognition domain (ARD) have not been previously evaluated in a retrospective analysis. During a prior grant period, a collaborative project was launched with the research laboratory at the Georgetown University Medical Center to generate complete HLA gene sequencing at HLA-A, B, C, DRB1, DQB1 and DPB1 on a cohort of previously characterized ARD identical at HLA-A, B, C, DRB1 and DQB1 unrelated donor/recipient pairs from the CIBMTR research repository.

A pilot cohort of 360 pairs were analyzed to assess the frequency of sequence disparities outside of the ARD and facilitate a sample size calculation for the final study cohort. The majority of the population was self-identified Caucasian (80%). NGS was performed on the Illumina MiSeq platform and interpreted with Connexio Assign MPS. Class I gene sequences covered 5'UTR-3'UTR; DRB1, intron 1-intron 3; DQA1 5'UTR-exon 4; DQB1, intron 1-3'UTR. DQ noncoding regions were not evaluated. The majority (98.1%) of the pairs were matched for sequences outside the ARD exons: 0.5% differed in non-ARD exons, 1.9% differ in noncoding regions. A small number (0.2%) differed within ARD exons. Mismatches in non-ARD exons varied from 0.7% for HLA-C and DQA1 to 0% DQB1; noncoding variation ranges from 2.8% for HLA-C to 1.3%, HLA-B and DRB1. Within non-ARD exons, both nonsynonymous (16 allele pairs) and silent (2) variation were present. Intron variation was minor and usually impact only a single nucleotide. The results of the initial study were presented as an ASHI Scholar award winning oral abstract during the 2016 ASHI annual meeting and was published in HLA[20].

To extend these findings was continued the study in a larger cohort. Full-length HLA Class I allele sequences (HLA-A, -B, -C) and partial-length (partial intron 1 through partial intron 3) Class II allele sequences (HLA-DRB1, DQB1) were compared for 4,646 high-resolution 10/10 HLA-matched HCT donor-recipient pairs using a comprehensive HLA allele sequence comparison pipeline. The sequence analysis pipeline identifies and annotates the mismatched positions between two alleles by their functional region and their protein sequence differences using IMGT/HLA Database (v3.31.0).

In this larger cohort, we found that for HLA Class I alleles, 95.4% of the ARD matched alleles have identical sequences outside the ARD, including introns and non-ARD exons. 0.3% of the mismatches were synonymous variants from the ARD region while 0.2% and 0.1% of mismatches found from non-ARD exons were synonymous and nonsynonymous variants, respectively. The intronic variation accounted for 4.2% of the mismatches. Similarly, for HLA Class II alleles, 0.3% of mismatches were synonymous ARD variants, and the mismatches in the non-ARD exons were also very rare (synonymous: 0.3%; nonsynonymous: 0.2%). However, due to the high polymorphism in the intronic regions of the Class II genes, 26.5% of mismatches were intronic, and only 77.3% of allele pairs shared identical sequences. 0.2% and 4.6% of Class I and Class II allele pairs, respectively, showed both exonic and intronic mismatches (Figure 12).

This analysis confirmed that HCT donor/recipient pairs matched at high resolution for HLA-A, B, C, DRB1 and DQB1 have limited coding variation outside of the ARD. Intronic variation was observed at a higher rate, but these non-coding differences are unlikely to influence alloreactivity as they do not contribute to the final protein structure. The results of this analysis were submitted as an abstract to the 2018 ASHI annual meeting.

Assessment of non-ARD mismatches and impact on clinical outcome will require larger datasets due to the low frequency of coding variant mismatches. This study population will continue to be extended as data is generated through the Donor Recipient Pair Project (DRPP).

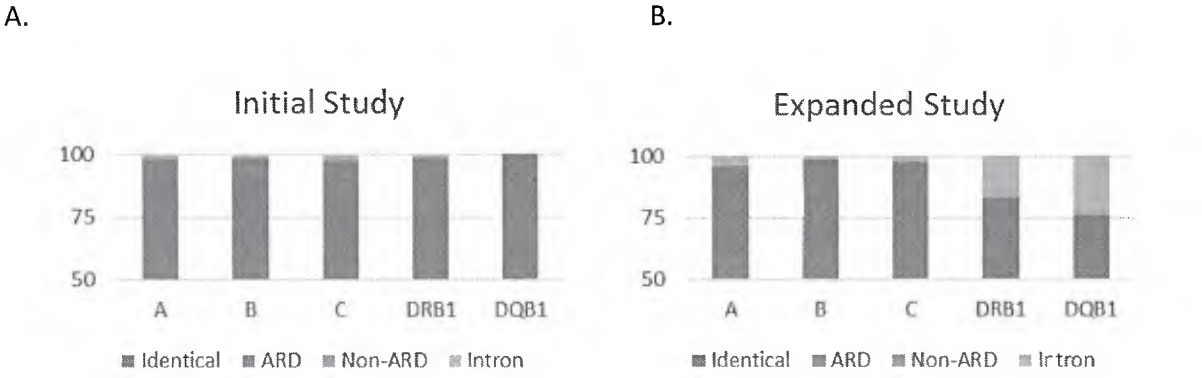


Figure 12. Summary of HLA matching between unrelated donor and recipient by locus. The four categories include: (1) donor and recipient carry identical alleles (exons and introns); (2) donor and recipient exhibit a difference in the exons encoding the ARD; (3) donor and recipient exhibit a difference in the non-ARD encoding exons; and (4) donor and recipient exhibit a difference in an intron. Chart A represents 720 allele comparisons while chart B represents 9,292 allele comparisons.

Donor/Recipient Pair Project KIR

While HLA matching is the most critical genetic determinant of HCT success, studies have found additional genetic determinants that may incrementally impact outcomes – for example, a correlation between KIR B content and relapse-free survival in AML[17]. However, interpretations of association studies are complicated because the underlying haplotypic structures have not been elucidated. In particular, copy number ambiguities need to be investigated further. Only when these haplotypes are understood can more powerful association studies be conducted. More studies are needed to evaluate the roles of non-HLA loci in HCT. KIR presence/absence typing has been included with the majority of the DRPP sample groups since 2009. To date, more than 16,000 pairs where either the donor, recipient or both have been presence/absence typed.

Production of the KIR SAVE dataset

In 2016 a dataset was developed to archive all available KIR data received from research projects or through the DRPP on both donors and recipients. The KIR data contained within this dataset ranges from allelic, copy number variation to presence absence of the KIR2DL1-5, 2DS1-5, 3DL1-3, 3DS1, 2DP1 and 3DP1. The dataset includes variables that define KIR ligand match grades, the assignments of the haplotypes into A and B containing regions as well as the Cooley KIR-B content scores and assignments. The KIR SAVE dataset is refreshed bi-annually

to incorporate KIR and HLA data generated through the DRPP and other research projects. The dataset is the primary source for KIR analyses within the CIBMTR.

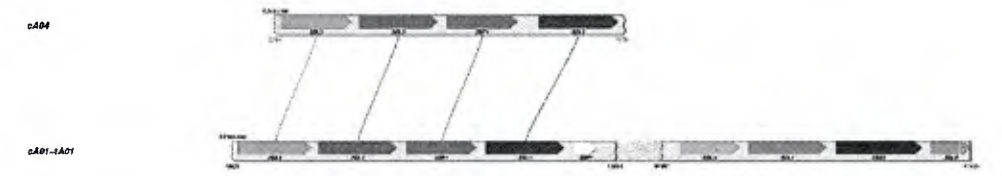
Full KIR region sequencing

The most informative way to characterize the full KIR region is to sequence it from long single molecules. These whole region sequences provide the ability to experiment, discover, and annotate at the highest level of resolution. They also provide indirect value as references, evolutionary informers, and source material for imputation.

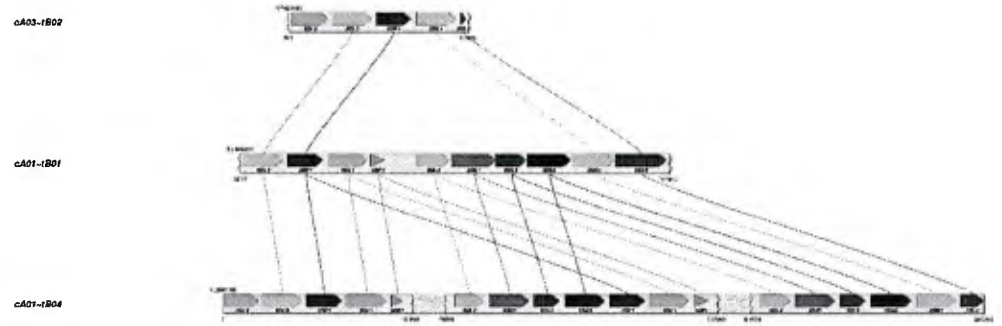
A collaborative study with Scisco Genetics and Pacific Biosciences was developed to perform full KIR haplotype sequencing. KIR haplotypes were prepared via fosmid library construction, including content mapping and fosmid isolation followed by DNA sequencing of the fosmid clones using Pacific Biosciences long read sequencing technology.

This method allowed, for the first time, the generation of comprehensive phased sequence of sixteen *KIR* haplotypes from eight individuals without imputation. The individuals had previously been typed at presence/absence, copy number, and SSO/SSP in the exons[31]. The group was chosen for a balance of known/unknown haplotypes, insertion/deletion events, A/B content, and representation of the centromeric and telomeric regions. The results revealed four novel haplotype structures, a novel gene-fusion allele, novel and confirmed insertion/deletion events, a homozygous individual, and overall diversity for the structural haplotypes and their alleles. The haplotype sequences and gene annotations provide alternative loci for the *KIR* region in the human genome reference. The results of the analysis are summarized in Figure 13 and Table 4 and were published in *Genes & Immunity*.

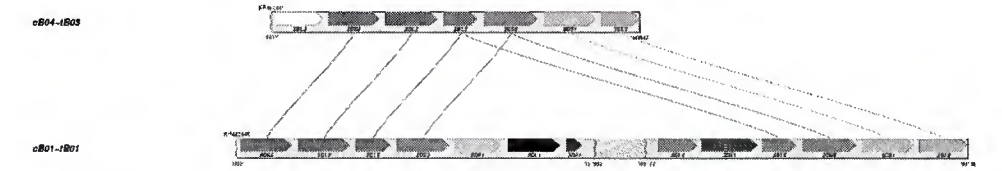
a)


cA04
cA01-tA01

b)


cA03-tB02
cA01-tB01
cA01-tB04

c)


cB04-tB03
cB01-tB01

d)

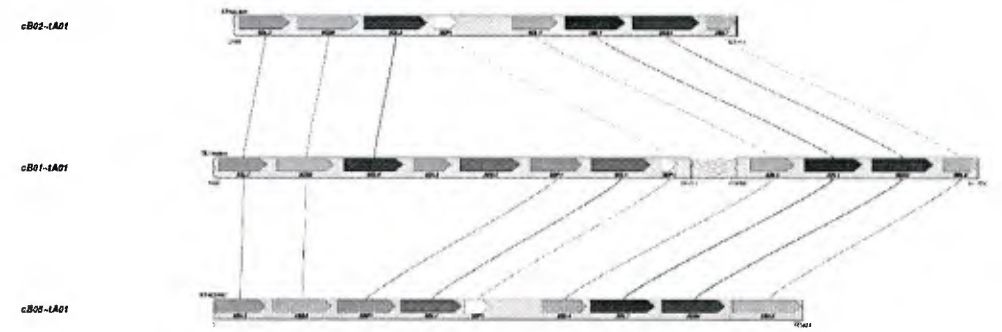

cB02-tA01
cB01-tA01
cB03-tA01

Figure 13. Haplotype structures and regional motifs. Each of the nine structural haplotypes is depicted within the context of pairs of centromeric/telomeric regions and A/B motifs: a) cAXX~tAXX b) cAXX~tBXX c) cBXX~tBXX d) cBXX~tAXX. cB01~tA01 was previously published and is included to provide the cBXX~tAXX reference. Haplotypes cA01~tB01 and cB01~tB01 contain KIR3DL3 but were not captured in the fosmid.

Table 4. Novel alleles by gene and resolution. Each of the 16 genes is broken down by frequency of partial alleles and three levels of annotation: protein, CDS, and full-gene. KIR2DP1 and KIR3DP1 are pseudogenes.

Gene	# Alleles	% Partial sequence	% Novel protein	% Novel CDS	% Novel full gene
KIR2DL2	3	0%	0%	0%	100%
KIR2DL3	11	0%	0%	0%	100%
KIR2DL4	13	0%	15%	15%	100%
KIR2DL5	6	0%	0%	0%	100%
KIR2DP1	14	0%	50%	50%	86%
KIR2DS1	5	0%	20%	20%	100%
KIR2DS2	4	0%	0%	0%	100%
KIR2DS3	3	0%	0%	0%	100%
KIR2DS4	9	0%	11%	11%	89%
KIR2DS5	3	0%	0%	0%	100%
KIR3DL1	9	0%	22%	22%	89%
KIR3DL2	14	64%	7%	14%	36%
KIR3DL3	13	23%	8%	8%	77%
KIR3DP1	13	0%	69%	69%	77%
KIR3DS1	4	0%	0%	0%	0%

17th International Histocompatibility and Immunogenetics Workshop (IHIW) collaboration

The NMDP collaborated with the IHIW KIR component to produce multiple replicates of a panel of 10 KIR defined reference samples from the pool of previously expanded high resolution KIR typed cell lines at the CIBMTR research repository. The sequences were used as "ground truth" KIR portion of the 17th Workshop. The panel was used to qualify laboratories for participation in the IHIW KIR sequencing project. Laboratories received either DNA or viable cell lines as requested. The samples were selected for haplotypic diversity and alleles with large insertions and/or deletions. We received presence absence typing from 7 of the 9 typing labs and CNV typing from 4. We have also started a collaboration with the DKMS typing laboratory in Dresden to confirm the allelic typing on 40 NMDP KIR high resolution typed reference cell lines. These results were presented at the 17th IHIW meeting in September 2017.

Non-Antigen Recognition Domain (ARD) Mismatch study

Amino acid mismatches outside the ARD (i.e., exons 2 and 3 for HLA class I and exon 2 for class II) are ignored under current HLA matching guidelines with the assumption that these differences are irrelevant. There is little data to confirm or refute this assumption; furthermore, the amount of data needed to form a conclusion is unattainable.[24] In order to provide more information, the ARD allo-reactivity assessment project will provide insight into the allowable percent tolerance of matching needed outside of the ARD. It is collaboration between the NMDP and Europdonor under the direction of Machteld Oudshoorn and Franz Claas from Leiden, Netherlands.

Initial investigation of the Class II ARD mismatch of DRB1*14:01 and DRB1*14:54 and DRB3*02:01 and 02:02 respectively have produced preliminary results demonstrating two weakly positive and one positive result. Interestingly, all positive results occurred in one direction only, which is DRB1*14:01 / DRB3*02:01 against DRB1*14:54 / DRB3*02:02. This data from the Cass II analysis was presented in an oral abstract[19] at the 2013 EFI conference in Maastricht, Netherlands. To confirm these results, we identified 135 additional donors via registry queries. Fresh blood draws were collected from 22 donors and peripheral blood mononuclear cells cryopreserved for evaluation. All combinations tested showed no responses in the mixed lymphocyte culture whereas 4 out of 10 combinations were positive in the Elispot against the combined DRB1/DRB3 mismatch and only in one direction; DRB1*14:01/DRB3*02:01 against DRB1*14:54/DRB3*02:02. Positive responses were confirmed by primed lymphocyte testing (PLT) that was more sensitive than the Elispot. Furthermore, the PLT results suggested that the DRB1* mismatch was responsible for the response. In conclusion, mismatches involving positions outside the ARD are not very immunogenic. However, some mismatches can lead to T cell reactivity in vitro. The impact of

these mismatches on clinical outcome of HCT remains to be established. The study was published in Bone Marrow Transplantation.

Non-Antigen Recognition Domain (ARD) Mismatch study

Analysis of four HLA Class I ARD mismatches; A*02:01 and 02:09, B*44:02 and 44:27, C*07:01, 07:06 and 07:18 have shown that the selected pairs do not travel on the same haplotypes. A manuscript describing these results is under review in the Journal of Human Immunology.

IIC.2 Objective 2

Even when patient and donor are HLA matched, GVHD occurs, therefore, other loci may play a role.

Table 5 lists currently active and completed CIBMTR/NMDP-supported studies that are conducted on NMDP samples. The CIBMTR/NMDP encourages such collaborative projects and closely monitor them. Such studies are instrumental to understanding the role of non-HLA loci in HCT. The data is obtained and generated via NMDP donor and recipient research samples, along with their outcomes and demographics. The researchers are required to submit the interpreted results of all assays performed on the samples. The data submission requirement ensures that all sample testing yields information that is readily available to the HCT research community for subsequent analysis and eliminates or reduces duplicative testing to preserve resources and sample inventory. These results are stored in the IPR and IIDB databases, and associated with their samples in the CIBMTR Research Repository database.

Non-HLA data is available for use in research studies in a fashion analogous to the Donor/Recipient Pair Project generated HLA data and is made available, when possible, via the NMDP Bioinformatics web site. Data origin will be noted for all information stored, along with relevant citations. Access to the detailed data will be subject to the existing NMDP/CIBMTR data request procedures.

Table 5. Immunobiology typing projects utilizing NMDP samples and contributing data to the IPR database

Study Title	Investigator	Number of Samples	Genes of interest	Testing Method	Data submitted
NK Cells, Their Receptors and Unrelated Donor Transplant	J. Miller	2300 pairs	KIR	RT-PCR, FACS, SSO, MALDI-TOF	Yes
Survey of Diversity of Immune Response Genes in Unrelated Hematopoietic Stem Cell Transplantation	C. Hurley	40 Pairs	cytokine and KIR	SBT	Yes
Candidate Gene Study to Examine the Impact of Chemokine and Chemokine Receptor Gene Polymorphisms on the Incidence and Severity of Acute and Chronic GVHD	R. Abdi	1300 pairs	CCL1, CCL2, CCR5, CCR2, CX3CR1	Taqman PCR	Yes
Functional Significance of Killer Ig-like Receptor (KIR) Genes in HLA Matched and Mismatched Unrelated HCT	B. Dupont, K. Hsu	2000 pairs	KIR	SSP	Yes
Functional Significance of Cytokine Gene Polymorphism in Modulation Risk of Post-Transplant Complications	E. Petersdorf	2500 pairs	>30 Immune response genes	Taqman PCR	Yes
Identification of Functional SNPs in Unrelated HCT	E. Petersdorf	3500 pairs	Entire MHC region	Taqman PCR	In Process
Use of Female Donors with Pre-existing Antibody to H-Y Antigen will Result in Robust Serologic Response to H-Y Antigens in Male HSC transplantation Recipients	D. Miklos	288 pairs	H-Y Antigen	ELISA, protein array	Yes

Study Title	Investigator	Number of Samples	Genes of interest	Testing Method	Data submitted
Multiplexed Genotyping of Human Minor Histocompatibility Antigens (mHAg): Clinical Relevance of mHAg Disparity in Stem Cell Transplantation	T. Ellis	730 pairs	mHAg	Allele-specific Primer Extension	Yes
Genetic Polymorphisms in the Genes Encoding Human Interleukin-7 Receptor-a: Prognostic significance in Allogeneic Stem Cell Transplantation	K. Muller	851 pairs	IL-7	Taqman PCR	Yes
The Effect of Non-Inherited Maternal Antigens in Cord Blood Transplantation	L. Baxter-Lowe	102 pairs	HLA	SBT	Yes
Detection of HLA Antibody in Single Antigen HLA-Mismatched Unrelated Donor Transplants	S. Arai, D. Miklos	200 pairs	Anti-body	ELISA, Protein array	Yes
Detection of Donor-Directed, HLA-Specific Alloantibodies in Recipients of Unrelated Stem Cell Transplantation and Their Relationship to Graft/Patient Outcome	R. Bray	111 pairs	Anti-bodies	Flow cytometry	Yes
Genome-wide Association in Unrelated Donor Transplant Recipients and Donors: A Pilot Study	R. Goyal	858 pairs	> 600,000 Genome wide SNPs	Human 610 - Quad V1 arrays	Yes
SNPs in the p53 Pathway and Outcomes in URD HCT	B. DuPont	1500 pairs	p53, ATM, MDM2 and p21/Waf1	Taqman	In process

Study Title	Investigator	Number of Samples	Genes of interest	Testing Method	Data submitted
Association of Donor and Recipient Gene Polymorphisms of Drug and Innate Immune Response with Outcomes after URD HCT	V. Rocha	725 pairs	GSTP, GSTT, GSTM, UGT CD14, TIRAP, and NALPs	Taqman	Yes
To Develop and Test a Prognostic Index for Survival in CML URD HCT	A. Dickinson	1100 pairs	TNF, IL-1RA and IL-10	Taqman	Yes
Evaluation of TGF-β1 Promoter and Signal Peptide Polymorphisms as Risk Factors for Renal Dysfunction in HCT Patients Treated with Cyclosporine A	R. Shah	400 samples	TGF-β1	Taqman	Yes
Donor and Recipient Telomere Length as Predictors of Outcomes after Hematopoietic Stem Cell Transplant in Patients with Acquired Severe Aplastic Anemia	S. Gadalla	650 samples	Telomere length and Telomerase Polymorphisms	Taqman	Yes
Development of a GVHD Prevention Biodiagnostic Test	R. Somogyi	450 samples	Gene Expression Array	Array	Yes
Genetic polymorphisms and HCT related mortality Re: Pre-HCT conditioning in matched unrelated donor HCT	T. Hahn	>4,000 pairs	GWAS	Array	In process
Impact of CTLA4 SNPs on outcome after URD transplant	M. Jagasia	1,200 pairs	CTLA-4 SNPs	Taqman	Yes
KIR genotyping and immune function in MDS patients prior to unrelated donor transplantation	E. E.Warlick and J. Miller	970 samples	KIR genotype, expression and cellular function	SSP, flow cytometry and cellular assays	Yes

Study Title	Investigator	Number of Samples	Genes of interest	Testing Method	Data submitted
Plasma YKL-40 and CHI3LI genotype to predict mortality after unrelated donor HCT	B. Kornblit	800 pairs	YKL-40 plasma levels and CHI3LI SNPs	ELISA and Taqman	Yes
Natural killer cell genomics and outcomes after allogeneic transplantation for lymphoma	V. Bachanova, J. Miller, D. Weisdorf and L. Burns	800 pairs	KIR genotype, expression and cellular function	SSP, flow cytometry and cellular assays	Yes
Effect of genetic ancestry matching on HCT outcomes	A. Madbouly, M. Maiers and N. Majhail	2300 pairs	Ancestry Informative Markers	Taqman GWAS	Yes
Impact of MHC Class I chain related polymorphisms on HCT outcomes	M. Askar and R. Sobecks	700 pairs	MICA genotypes	Taqman	Yes
Prognostic impact of somatic mutation and the levels of CXC chemokine ligands in MDS	W. Saber, R.C. Lindsley and B. Ebert	1300 pairs	Chemokine levels Somatic mutations	ELISA Sequence capture	Yes
Mitochondrial DNA haplotypes and outcome	M. Verneris and J. Ross	4000 pairs	SNPs	Taqman	Yes
Assessing T cell repertoire similarity in HLA mismatched HCT	E. Meyer	50 samples	TCR repertoire sequence	NGS	In process
Impact of SNPs in the Gamma Block of the MHC	M. Askar and R. Sobecks	700 pairs	SNPs	Taqman	Yes
Clinical outcomes among HCT recipients as a function of socioeconomic status and transcriptome differences	J. Knight, J.D. Rizzo and S. Cole	252 samples	Gene expression array	Array	Yes
Natural killer cell genomics and outcomes after HCT for CLL	V. Bachanova, J. Miller, D. Weisdorf and S. Cooley	600 samples	KIR genotype	SSP	Yes

Study Title	Investigator	Number of Samples	Genes of interest	Testing Method	Data submitted
Donor telomere length and outcomes after HCT for acute leukemia	S. Gadalla, S. Savage, D. Loftus and E. Hytopoulos	1145 samples	Leukocyte telomere length	qPCR	Yes
KIR gene content and pediatric acute leukemia HCT outcome	M. Verneris, J. Miller and S. Cooley	500 samples	KIR genotype	SSP	In process
Functional genetic variants of the ST2 gene in pairs of recipient and donors for risk stratification of GVHD and TRM outcomes.	S. Paczesny and S. Spellman	1000 pairs	sST2	Taqman	Yes
The role of HLA-E compatibility in the prognosis of acute leukemia patients undergoing 10/10 HLA matched HCT	C. Tsamadou, D. Furst and J. Mytilineos	3300 pairs	HLA-E	NGS	In process
Donor-Recipient NK cell determinants associated with survival in JMML after HCT	D. Lee, H. Rangarahan	465 pairs	KIR	NGS	In process
Identification of genomic markers of post-HCT outcomes in patients with myelofibrosis	W. Saber, S. Gadalla	393 samples	Somatic mutations	Taqman	In process
Epigenetic profiling of URD donor/recipient pairs to improve donor selection for HCT	S. Beck, K. Peggs, V. Rakyan, A. Webster	288 pairs	DNA methylation	EPIC array	In process
Impact of telomere length and telomerase gene mutations on allogeneic stem cell transplantation in myelodysplastic syndrome	C. Lindsley, I. DeVivo, S. Agrawal, D. Neuberg	1300 pairs	Telomere length and telomerase gene mutations	RT-PCR Taqman	In process

Clinical Research in Transplantation

Clinical research in transplantation improves transplant outcomes and supports preparedness for a contingency response.

Clinical Outcomes Research

Clinical outcomes research using the CIBMTR research database is a core activity of the organization. These studies address a wide range of issues, focusing on questions that are difficult or impossible to address in single center studies or randomized trials because diseases treated with HCT are uncommon, single centers treat few patients with a given disorder, and not all important questions are amenable to a randomized research design. The majority of the clinical outcomes research is conducted through the CIBMTR WC structure, which incorporates many highly successful researchers in clinical transplantation. The WC perform retrospective studies to identify the most promising transplant approaches, and by identifying the patients most likely to benefit from this therapy. In addition, research in immunobiology was conducted to better understand how transplantation works including how to harness the power of the immune system to control cancer.

The CIBMTR collects data for approximately 24,000 new transplant recipients annually as well as a continually increasing volume of follow-up data on previously reported recipients and donors. Figure 14 shows cumulative accession of transplants since 1970 when the International Bone Marrow Transplant Registry began collecting these data. These data are the basis for the CIBMTR Clinical Outcomes Research program and are accessed by the WC to conduct studies.

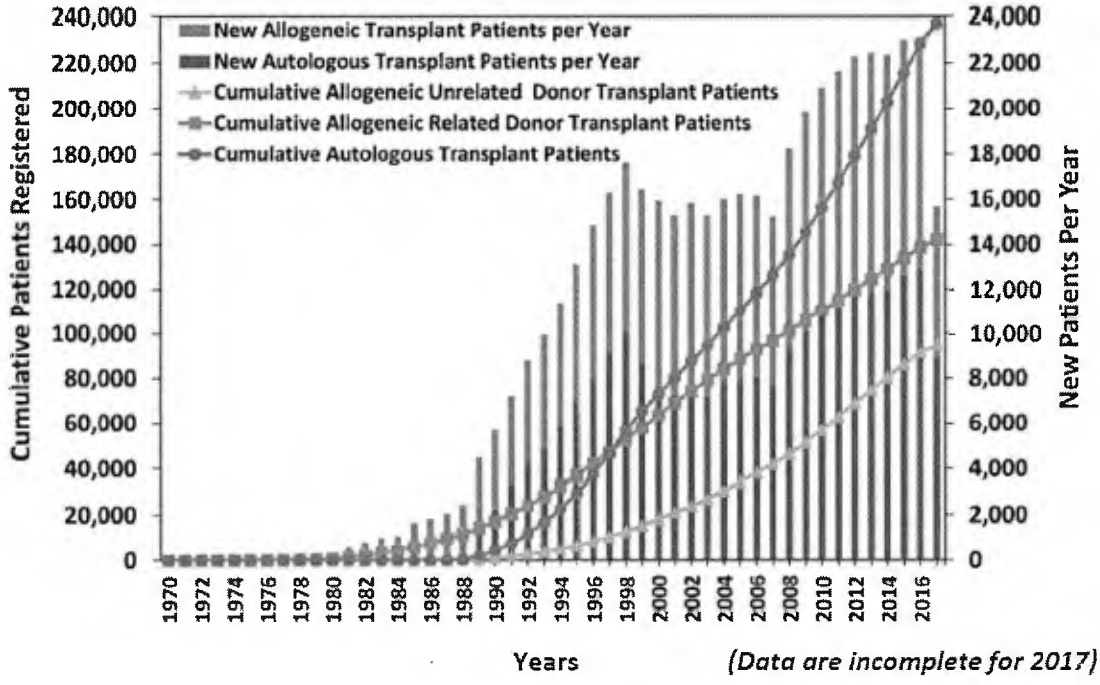


Figure 14. Accession of Transplant Recipients Registered with the CIBMTR

Currently, there are 15 WC within the CIBMTR with 175 active studies in progress (Table 6). In 2017, the CIBMTR published a total of 82 mostly peer-reviewed publications (59 working committee studies, 2 Health Services Research, 7 BMTCTN, 4 Statistical Methods and 10 Bioinformatics) (Figure 15). Sources of funding for these studies vary by investigator, but the majority use NMDP resources and CIBMTR statistical support. In addition, the CIBMTR received 207 new study proposals and accepted 80 for discussion at the February 2018 ASBMT/CIBMTR Transplant Tandem Meetings (renamed the Transplant and Cellular Therapy Meeting for 2019). Proposals can be dropped for various reasons including; feasibility, low scientific impact, overlap with existing studies or combined with other proposals due to overlapping hypotheses. The working committees presented 30 abstracts (17 oral and 13 poster) at national and international meetings in 2017. The activity of each working committee for 2017 is summarized in Table 6.

Table 6. 2017 CIBMTR Working Committee portfolio and productivity

Working Committee	Studies in Progress	Publications	Presentations
Acute Leukemia	13	6	2 (1 oral / 1 poster)
Autoimmune Diseases and Cellular Therapies	5	1	0 (0 oral / 0 poster)
Chronic Leukemia	12	3	3 (2 oral / 1 poster)
Donor Health and Safety	13	2	1 (0 oral / 1 poster)
Graft Sources and Manipulation	7	3	1 (1 oral / 0 poster)
Graft-versus-Host Disease	13	3	2 (1 oral / 1 poster)
Health Services and International Studies	10	2	0 (0 oral / 0 poster)
Immunobiology	38	10	5 (1 oral / 4 poster)
Infection and Immune Reconstitution	7	0	1 (0 oral / 1 poster)
Late Effects and Quality of Life	13	6	4 (4 oral / 0 poster)
Lymphoma	10	6	3 (3 oral / 0 poster)
Pediatric Cancer	1	3	0 (0 oral / 0 poster)
Plasma Cell Disorders and Adult Solid Tumors	8	7	3 (1 oral / 2 poster)
Primary Immune Deficiencies, Inborn Errors of Metabolism, and Other Non-Malignant Marrow Disorders	13	4	1 (0 oral / 1 poster)
Regimen-Related Toxicity and Supportive Care	12	3	4 (3 oral / 1 poster)
TOTAL	175	59	30

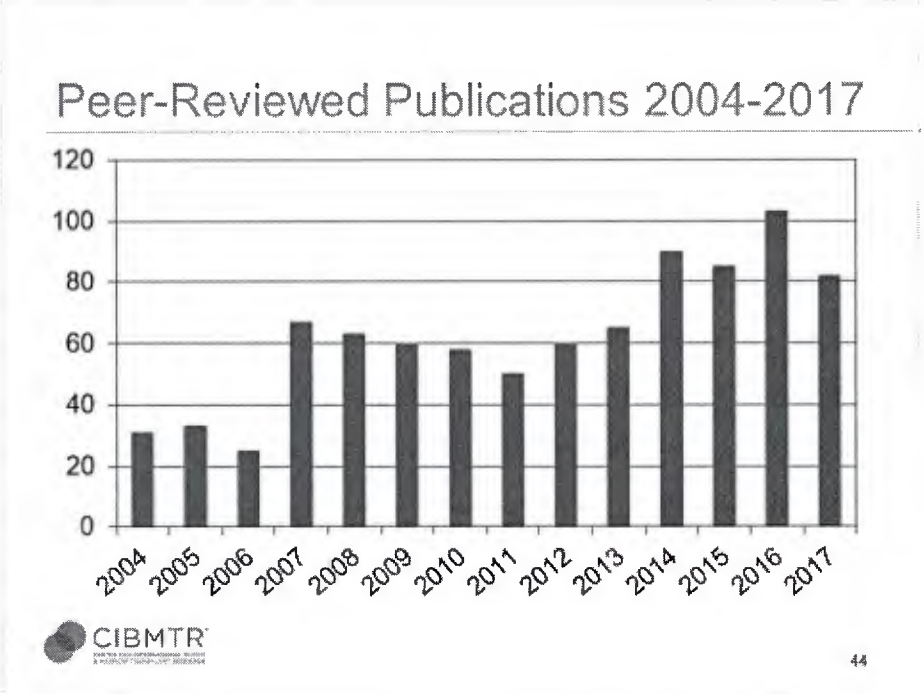


Figure 15. CIBMTR peer-reviewed publications by year.

Clinical Trials

In October 2010, RCI BMT activated a study referred to as the Long Term Donor Follow up study. The primary goal of this study is to evaluate the hypothesis that the incidence of targeted malignant, thrombotic and autoimmune disorders after unrelated hematopoietic stem cell donation are similar between unstimulated BM and filgrastim-mobilized PBSC donors. Once the donor has consented to participate, the donor is contacted and asked study specific questions every other year. This will continue until study completion which is estimated to be 2020. If the donor reports an incidence of interest, a request for their medical records is made. Cases of targeted disorders are reviewed by the medical monitors to confirm the veracity of the report.

In October 2015, accrual to this study was closed; however, follow-up assessments will continue until the end of 2020. Table 7 summarizes the accrual by cohort and product. The SRG team is responsible for the follow up assessments of just over 63% of the enrolled donors. To-date, the SRG has completed a total of 36,941 assessments of which 6,009 were during this past year.

Table 7. Long Term Donor Follow-up Study accrual summary

	Marrow	PBSC	Both	Total
Prospective	3009	8904	170	12083
Retrospective	3852	5478	381	9711
Totals	6861	14382	551	21794

Other Clinical Research activities

In 2014, we explored options for a) comprehensive system for management of activities and studies within the SRG and b) electronic data capture system (EDC) and CTMS to coordinate operational and administrative activities within RCI BMT. In March 2015 the SRG call tracking system built within SalesForce platform went into production. In June 2015, we initiated work on implementing Medidata RAVE for our EDC system and their CTMS solution for our internal trial management activities. In 2018, we explored options and began implementing a solution for an eTMF (electronic Trial Master File) system to efficiently store clinical regulatory documents in compliance with FDA regulations.

SRG solution

Fully implemented Medidata RAVE for electronic data capture system and a CTMS. During the past year all study management has been transitioned to the CTMS. Currently there are a total of 3 trials in RAVE with an additional 3 studies in process of design/build. In addition to multi-center trials, CIBMTR is also utilizing RAVE to collect supplemental data for observational studies or for corporate projects when appropriate One supplemental data project currently resides in RAVE with three supplemental data collection projects in discussion.

Patient Reported Outcomes (PRO) system within SRG:

Numerous studies now recognize the value of measuring PROs as the most accurate measure of the patient's experience with disease and treatment, primary and secondary outcomes in clinical trials, and 'biomarkers' of disease activities. Several studies in HCT show that pre-HCT PROs can predict survival and post-HCT health related quality of life (HRQoL). Collecting PRO data will allow CIBMTR to conduct research in HCT outcomes that are important to patients and their caregivers. Collecting PRO with an electronic system will allow for the most direct, cost effective and efficient way to collect this important data. In 2017, the team determined the requirements of a system and explored potential solutions, inclusive of use of Patient-Reported

Outcomes Measurement Information System (PROMIS®) measures. PROMIS is a set of person-centered measures that evaluate and monitor physical, mental and social health in adults and in children. It is important for the selected system to also allow other measures to be incorporated into the surveys and be flexible and easy access for patients, donors and research subjects. A recommendation was presented to CIBMTR leadership and an initial proof of concept executed in 2017. The initial ePRO pilot study will launch in May/June 2018, utilizing the interaction among the PROMIS measures, Qualtrics (patient interface), Salesforce (CRM system) and IDW (CIBMTR's outcomes database). Following execution of the study, the system will be assessed for more broad utilization.

Cord Blood Research Initiatives

During the project period, the Cord Blood Research Sub-advisory Group met semi-monthly to discuss study priorities and plan analyses for the following:

Colony Forming Unit – State of the Science

Cord blood banks (CBB) regard the colony forming unit (CFU) assay as an important way to measure the quality of a cord blood unit. The CBBs recognize that transplant centers generally have insufficient knowledge of the assay to incorporate the results appropriately into their selection practices. Therefore, the Cord Blood Advisory Group deemed that CBBs are responsible for educating their clinical colleagues. As a result, members of the Cord Blood Advisory Group began preparation of a CFU State of the Science manuscript with the intent of describing CBB practices and assay indications to help establish informed transplant center applications. The group also submitted an abstract on the topic to the AABB International Cord Blood Symposium that received a best abstract award. The manuscript will be submitted during the current grant period.

NMDP Cord Blood Access (10-CBA) Protocol Clinical Results

Umbilical cord blood transplantation (UCBT) is an important option for patients, including those of diverse race/ethnicity, without a matched donor. The FDA began licensure of UCB units in 2011. Fewer than 5% of UCB units are licensed; therefore, the NMDP facilitated UCBT under IND: "A Multicenter Access and Distribution Protocol for Unlicensed Cryopreserved Cord Blood Units for Transplantation in Pediatric and Adult Patients with Hematologic Malignancies and Other Indications." The CIBMTR analyzed and presented outcomes of 1589 patients undergoing UCBT using unlicensed units. Engraftment and overall survival were excellent for the diverse patients receiving UCBT using these unlicensed units. Incidence of neutrophil engraftment (ANC > 500) at Day 42 was 88%, 89%, and 92% for adults, pediatric-malignant disease (PediM), and pediatric non-malignant disease (pediNM) respectively (Figure 16). Overall survival (OS) at 100 days/1 year was 82% and 55% for adults, 86% and 67% for pediM, and 92% and 79% for pediNM (Figure 17). The results were presented as a poster at the 2017

BMT Tandem Meetings and as an oral presentation at the 2017 NMDP Council Meeting. A manuscript describing the results is currently under review in BBMT.

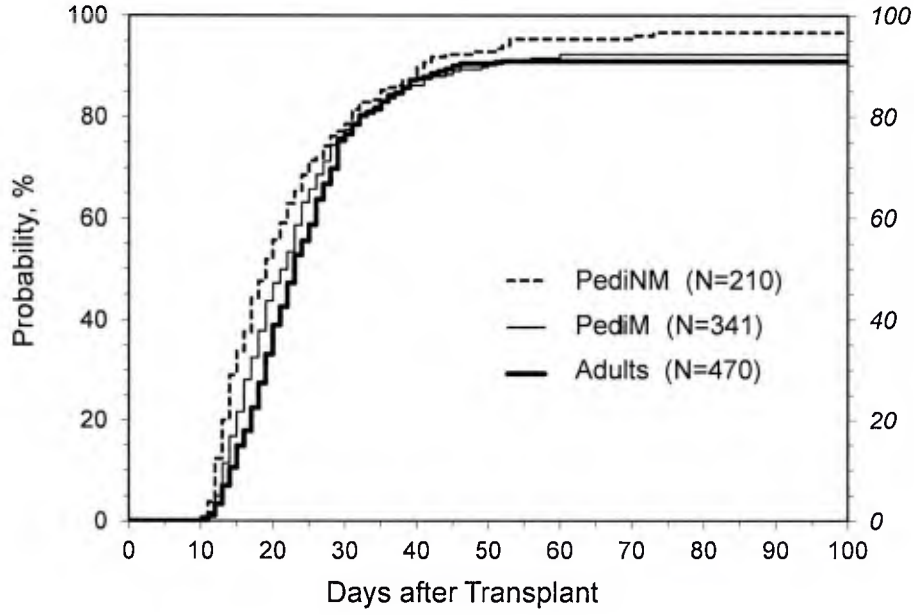


Figure 16. Neutrophil Engraftment after First Umbilical Cord Blood Transplantation (Myeloablative only)

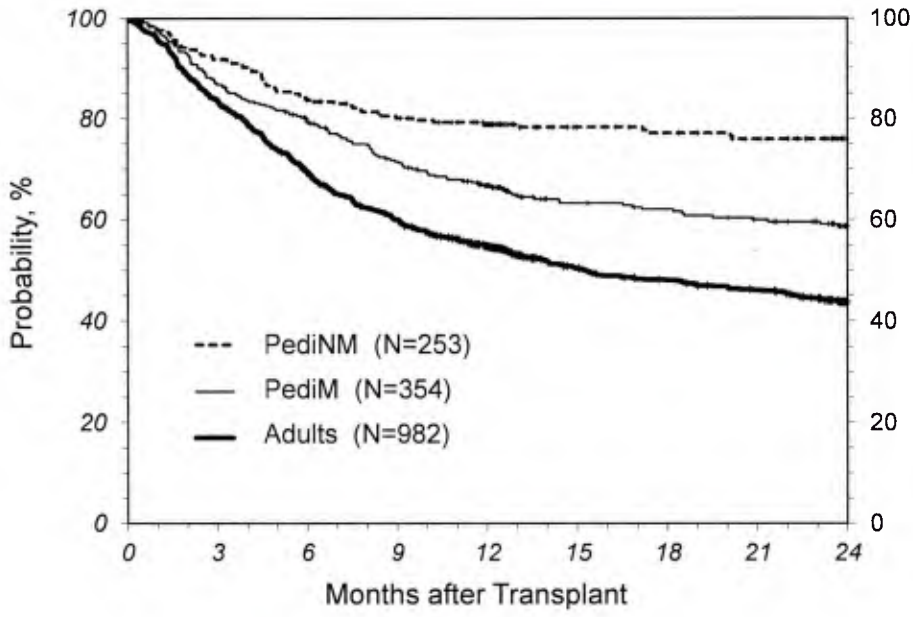


Figure 17. Overall Survival after First Umbilical Cord Blood Transplantation

Immunobiology Research

During a previous grant period, the NMDP developed the Immunobiology Research grant request and award procedures for use by the Immunobiology Working Committee (IBWC) and developed the IBWC Web site (http://www.cibmtr.org/COMMITTEES/Working_Committees/Immunobiology/index.html). The content was further refined and migrated to the CIBMTR.org Web site in 2010 and is refreshed annually.

During the past grant period, grant funds supported significant outreach efforts by the IBWC leadership to increase exposure for the IBWC to basic scientists. The IBWC leadership attended several scientific meetings including: American Society of Hematology, BMT Tandem, European Group for Blood and Marrow Transplant and American Society for Histocompatibility and Immunogenetics meetings. In addition, the assistant scientific director gave presentations on CIBMTR and IBWC research activities at the 3rd Annual Pujiang Symposium and the 2018 Data Management Professional meeting. Support permitted the committee to maintain a strong performance record with publications (submitted or accepted) and collaboration on 2 grants submitted in calendar year 2017. In addition, 5 new proposals were accepted by the IBWC during the 2018 BMT Tandem Meeting.

IBWC 2017-18 manuscripts (submitted/accepted):

1. **IB08-08** Goyal RK, Lee SJ, Wang T, Trucco M, Haagenson M, Spellman SR, Veneris M, Ferrell RE. Novel HLA-DP region susceptibility loci associated with severe acute GvHD. ***Bone Marrow Transplant 2017 Jan 1;52(1):95-100. doi:10.1038/bmt.2016.210. Epub 2016 Sep 5.***

2. **IB12-04** Hoff GA, Fischer JC, Hsu K, Cooley S, Miller JS, Wang T, Haagenson M, Spellman S, Lee SJ, Uhrberg M, Venstrom JM, Verneris MR. Recipient HLA-C haplotypes and miRNA 148a/b binding sites have no impact on allogeneic hematopoietic cell transplantation outcomes. ***Biol Blood Marrow Transplant* 2017 Jan 1; 23(1):153-160. doi:10.1016/ j.bbmt.2016.09.028. Epub 2016 Oct 13.**

3. **IB13-05** Askar M, Sobecks R, Wang T, Haagenson M, Majhail N, Madbouly A, Thomas D, Zhang A, Fleischhauer K, Hsu K, Verneris M, Lee SJ, Spellman SR, Fernández-Viña M. MHC class I chain-related gene A (MICA) donor-recipient mismatches and MICA-129 polymorphism in unrelated donor hematopoietic cell transplantations has no impact on outcomes in acute lymphoblastic leukemia, acute myeloid leukemia, or myelodysplastic syndrome: A Center for International Blood and Marrow Transplant Research study. ***Biol Blood Marrow Transplant 2017 March 1; 23(3):436-444. doi.org/10.1016/j.bbmt.2016.11.021. Epub 2016 Dec 14.***

4. **IB14-03b** Lindsley RC, Saber W, Mar B, Medd, Wang T, Haagenson M, Grauman P, Zhu Z, Spellman S, Lee SJ, Verneris M, Hsu K, Fleischhauer K, Cutler C, Antin JH, Neuberg D, Ebert BL. Prognostic Mutations in Myelodysplastic Syndrome After Stem Cell Transplantation. ***New Engl J Med 2017 Feb 9; 376(6):536-547. doi.org/10.1056/NEJMoa1611604. Epub 2017 Feb 9.***

5. **IB12-03** Madbouly A, Wang T, Haagenson M, Paunic V, Vierra-Green C, Fleischhauer K, Hsu KC, Verneris MR, Majhail NS, Lee SJ, Spellman SR and Maiers. Investigating the association of genetic admixture and donor/recipient genetic disparity with transplant outcomes. ***Biol Blood Marrow Transplant 2017 June 1; 23(6):1029-1037. doi.org/10.1016/j.bbmt.2017.02.019. Epub 2017 March 2.***

6. **IB15-06c** Wang Y, Wang T, Dagnall C, Haagenson M, Spellman SR, Hicks B, Jones K, Lee SJ, Savage SA, Gadalla SM. Relative telomere length before hematopoietic cell transplantation and outcome after unrelated donor hematopoietic cell transplantation for acute leukemia. ***Biol Blood Marrow Transplant 2017 July 1;23(7):1054-1058. doi.org/10.1016/j.bbmt.2017.03.032. Epub 2017 Apr 4.***

7. **R04-74e** Boudreau JE, Giglio F, Gooley TA, Stevenson PA, Le Luduec J-B, Shaffer BC, Rajalingam R, Hou L, Hurley CK, Noreen H, Reed EF, Yu N, Vierra-Green C, Haagenson M, Malkki M, Petersdorf EW, Spellman S, Hsu K. KIR3DL1/HLA-B subtypes govern acute myelogenous leukemia relapse after hematopoietic cell transplantation. ***J Clin Oncol 2017 July 10; 35(20).2268-2278. doi.org/10.1200/JCO.2016.70.7059. Epub 2017 May 18.***

8. **IB12-02B** Fleischhauer K, Ahn KW, Wang H-L, Zito L, Crivello P, Müller C, Verneris M, Shaw BE, Pidala J, Oudshorn M, Lee SJ and Spellman SR. Directionality of non-permissive HLA-DPB1 T-cell epitope group mismatches in 8/8 matched unrelated donor hematopoietic cell transplantation. ***Bone Marrow Transplant. doi.org/10.1038/bmt.2017.96. Epub 2017 June 5.***

9. **IB13-01** Eapen M, Wang T, Veys PA, Boelens JJ, St Martin A, Spellman S, Bonfim CS, Brady C, Cant AJ, Dalle J-H, Davies SM, Freeman J, Hsu KC, Fleischhauer K, Kenzey C, Kurtzberg J, Michel G, Orchard PJ, Paviglianiti A, Rocha V, Veneris MR, Volt F, Wynn R, Lee SJ, Horowitz MM, Gluckman E, Ruggeri A. Allele-level HLA matching for umbilical cord blood transplantation for non-malignant diseases in children: A retrospective analysis. ***Lancet Haematol 2017 July 1;4(7):e325-e333. doi.org/10.1016/S2352-3026(17)30104-7. Epub 2017 June 13.***

10. **IB09-06/RT09-04b** Clay-Gilmour AI, Hahn T, Preus LM, Onel K, Skol A, Hungate E, Zhu Q, Haiman CA, Stram DO, Pooler L, Sheng X, Yan L, Liu Q, Hu Q, Liu S, Battaglia S, Zhu X, Block AW, Sait SNJ, Karaesmen E, Rizvi A, Weisdorf D, Ambrosone CB, Tritchler D, Ellinghaus E, Ellinghaus D, Stanulla M, Clavel J, Orsi L, Spellman SR, Pasquini MC, McCarthy PL, Sucheston-Campbell LE. Genetic association with B-cell acute lymphoblastic leukemia in allogeneic transplant patients differs by age and sex. ***Blood Advances. 2017 Sept 8;1(20):1717-1728. doi.org/10.1182/bloodadvances.2017006023. epub 2017 Sept 12.***

11. **IB14-01** William BM, Wang T, Haagenson M, Fleischhauer K, Verneris M, Hsu KC, de Lima MJ, Fernandez-Vina M, Spellman SR, Lee SJ, Hill BT. Impact of human leukocyte antigen (HLA) alleles on outcomes of allogeneic transplantation for B-cell non-Hodgkin lymphomas: A Center for International Blood and Marrow Transplant Research analysis. ***Biol Blood Marrow Transplant. doi.org/10.1016/j.bbmt.2017.11.003. Epub 2017 Nov 16.***

12. **IB15-06a** Gadalla SM, Wang T, Loftus D, Friedman L, Dagnall C, Haagenson M, Spellman SR, Buturovic L, Blauwkamp M, Shelton J, Fleischhauer K, Hsu KC, Verneris MR, Krstajic D, Hicks B, Jones K, Lee SJ, Savage SA. Donor telomere length and outcomes after allogeneic unrelated hematopoietic cell transplant in patients with acute leukemia. ***Bone Marrow Transplant. doi.org/10.1038/s41409-017-0029-9. Epub 2017 Dec 21.***

13. **IB09-06/RT09-04** Ezgi Karaesmen, Abbas A. Rizvi, Leah Preus, Philip L. McCarthy, Marcelo C. Pasquini, Kenan Onel, Xiaochun Zhu, Stephen Spellman, Christopher A. Haiman, Daniel O. Stram, Loreall Pooler, Xin Sheng, Qianqian Zhu, Li Yan, Qian Liu, Qiang Hu, Amy Webb, Guy Brock, Alyssa I. Clay-Gilmour, Sebastiano Battaglia, David Tritchler, Song Liu, Theresa Hahn and Lara E. Sucheston-Campbell. Replication and validation of genetic polymorphisms associated with survival after allogeneic blood or marrow transplant **Blood 2017 :blood-2017-05-784637; doi: https://doi.org/10.1182/blood-2017-05-784637**

14. **IB13-08** Prediction of Acute Graft-Versus-Host Disease Following Hematopoietic Cell Transplantation (Lee C, Haneuse S, Wang H, Rose S, Spellman SR, Verneris M, Hsu K, Fleischhauer K, Lee SJ, Abdi R) ***In Press PLOS1.***

15. **IB15-06b** Evaluation of a Machine Learning-Based Prognostic Model for Unrelated Hematopoietic Cell Transplantation Donor Selection. Buturovic L, Shelton J, Spellman SR, Wang T, Friedman L, Loftus D, Hesterberg L, Woodring T, Fleischhauer K, Hsu KC, Verneris MR, Haagenson M, Lee SJ. ***In Press. Biol Blood Marrow Transplant.***

16. **IB09-06/RT09-04** Exomechip Analyses Identify Genes affecting mortality after HLA-Matched Unrelated Donor Blood and Marrow Transplantation Qian Liu, Qiang Hu, Leah Preus, Alyssa I. Clay, Ken Onel, Daniel O. Stram, Loreall Pooler, Xin Sheng, Christopher A. Haiman, Xiaochun Zhu, Stephen R. Spellman, Marcelo Pasquini, Philip L. McCarthy , Song Liu, Theresa Hahn, Lara E.

Sucheston-Campbell. ***Submitted. Blood.***

17. **IB10-01d** Flow Cytometry using FISH techniques in a Severe Aplastic Anemia population. Gadalla S, Aubert G, Wang T, Haagenson M, Spellman SR, Wang L, Katki HA, Savage S, Lee SJ. ***Submitted. Blood.***

18. **IB14-06** Donor-directed HLA-specific antibodies in unrelated hematopoietic cell transplantation for non-malignant disorders. Woolfrey A, Wang T, Lee SJ, Haagenson MD, Chen G, Fleischhauer K, Horan J, Hsu K, Tyan D, Verneris M, Spellman SR, Fernandez-Vina M. ***Submitted. Blood.***

19. **IB14-08** Development and validation of a clinical unrelated donor selection score. Shaw BE, Logan BR, Spellman SR, Marsh SGE, Robinson J, Pidala J, Hurley C, Barker J, Maiers M, Dehn J, Wang H, Haagenson M, Porter D, Petersdorf EW, Woolfrey A, Horowitz MM, Verneris M, Hsu KC, Fleischhauer K, Lee SJ. ***Submitted. Biol Blood Marrow Transplant.***

IBWC studies initiated in July 2017:

1. The impact of HLA-DPB1 levels of expression on clinical outcomes in HCT. PIs: M Askar and M Fernandez-Vina

2. Identification of genomic markers of post hematopoietic cell transplantation outcomes in patients with myelofibrosis. PIs: W Saber and S Gadalla

3. Donor-recipient NK cell determinants associated with survival in JMML after hematopoietic stem cell transplantation. PIs: D Lee and H Rangarajan

4. Epigenetic profiling of unrelated donor-recipient pairs to improve donor selection during hematopoietic stem cell transplants. PIs: S Beck, K Peggs, V Rakyan, A Webster

CIBMTR Information Technology (CIT) Minneapolis Initiatives

The scope of the work performed by the CIBMTR IT department in Minneapolis includes collecting and reporting outcomes data on all allogeneic transplantations performed in the U.S. (for the Stem Cell Therapeutic Outcomes Database (SCTOD), as required by U.S. law). U.S. transplant centers also voluntarily submit autologous transplantation data, and transplant centers worldwide voluntarily submit both autologous and allogeneic transplantation data. As a result,

and as reported in the CIBMTR 2016 Annual Report, the CIBMTR Research database now contains information on more than 475,000 patients. CIT strives to provide applications that will reduce center burden for government mandated forms and provide high quality data on demand.

CIT Application Suite:

- FormsNet: Recipient – Donor
- AGNIS
- Management Reporting
- Sample Tracking
- Auditing

FormsNet

Since its original release in Dec 2007, the Recipient Module of the FormsNet application has been used at more than 527 centers to register 214, 601 patients and collect over 1,741,961 forms with more than 10 million data elements. This program was developed for both local data entry from paper forms and web-based entry by clinical centers. More than 98% of data collected by the CIBMTR is submitted electronically via FormsNet. Two forms (2800 – log of appended documents and 2801 – transfer forms) can only be submitted on paper to ensure audit standards. The Form 2800 – log of appended documents, is in process of being decommissioned as a new feature has been added to FormsNet3 proving the ability to attach electronic documents directly to a form.

FormsNet 3.0 is CIBMTR's currently operational, 21 CFR Part 11 compliant, secure Web-based application for collecting hematopoetic cell transplant (HCT) outcomes data electronically. FormsNet supports data collection, auditing, and event reporting; donor clearance and follow-up; web services; and messaging. FormsNet offers real-time data validations; error messaging; and control of data entry flow, which includes enabling/disabling of questions and "smart navigation" between fields on a form. The system also collects information on non-HCT cellular therapies using a flexible design to accommodate therapies used independently, before or after HCT. The original deployment in December 2007 was built in 126,000 lines of code supporting 90 Recipient forms and no user tools. Today there are over 450,000 lines of code supporting 123 forms, tools, web services, email, and two user-based modules. Old revisions of Recipient and Donor forms are also still supported. The application is fully integrated with the CIT applications suite supporting CIBMTR. The application was converted from its original website to a web application with an enhanced object oriented code structure. Service Oriented Architecture integration services were created to provide flexibility and extensibility for future enhancements. In 2012, the planned upgrade to FormsNet replaced the technical foundation of the current FN2 application, with more agile, efficient & effective systems. It improved the user experience by providing enhanced functionality (defined by the network users). In 2014, the Donor module

was upgraded to the FormsNet 3 platform, providing the same benefits for Donor module users as realized by Recipient module users. In 2015, CIBMTR evaluated and determined that an external Clinical Trials product will be purchased and integrated with the CIBMTR platform to meet the electronic data capture business need, as opposed to an upgrade of the FormsNet application to support this need. Utilizing non-Navy funding, in 2016 the Medidata RAVE package was implemented for use as the web-based electronic data capture system for Clinical Trials and other prospective research projects. RAVE also is the system used for monitoring of the data submitted.

In 2017, FormsNet was upgraded quarterly to keep Recipient forms current with existing treatment practices. Eighteen revised Recipient forms were released into production, along with 3 new Recipient forms. Platform enhancement continued, including migration of the remaining 3 tools requiring conversion to FormsNet 3 from FormsNet 2 platform.

Continued to support data collection for the Myelofibrosis Medicare study; four new forms needed to support this study were released in January 2017.

Cellular Therapies: In 2017, implemented five cellular therapy form revisions and 3 new forms needed to support a cellular therapies registry.

Transitioned Infectious Disease Marker results from FormsNet1 (FN1) to FormsNet3 (FN3) in order to correct regulatory deficiencies, improve operational efficiencies and allow for the import of electronic results.

FormsNet was updated monthly during 2017 to enhance the Recipient, Donor, and Audit modules to apply enhancements and ensure optimal performance, flexibility and efficiency of applications.

A Growable Network Information System® (AGNIS)
AGNIS is a system for electronic messaging of standard Common Data Elements (CDEs) between participating nodes. Messaging can occur between transplant centers, registries, investigators or any combination of entities willing to map relevant data elements and install the software/messaging system. The system relies on two key components, data standards in the form of common data elements (CDEs), and software for transferring the data, providing audit trails, conveying error messages, etc.

- CDE Development:
  CIBMTR has invested substantial effort defining CDEs for CIBMTR forms. All CDEs are defined in the Cancer Data Standards Repository (caDSR) of the NCI. This leverages

a strong national system of standards regarding the definitions and related metadata. Additionally, a substantial portion of the CDEs have also been defined in the Biomedical Research Integrated Domain Group (BRIDG) model, which is compatible with HL7, the most prevalent 'language' used in biomedical informatics.

- Cancer Data Standards Repository (caDSR):
  - In the caDSR, common data elements for FormsNet database fields are compiled into Form Builder reports, which convert CIBMTR format into caDSR format and which centers use to submit data automatically to FormsNet via AGNIS. To date, common data elements have been created for nearly than 22,200 FormsNet database fields. This represents those database fields associated with 99% of the forms submitted via FormsNet. In addition, 40 Form Builder reports have been released in the caDSR, 71 are pending quality assurance testing in AGNIS, and 9 are pending testing by AGNIS end-users.

- Supported Forms:
  - 12 recipient outcome forms are available for electronic data exchange via AGNIS: five mandated forms (pre- and post-TED, HLA, IDM, Infusion), three Comprehensive Forms (Baseline, Follow-Up, and Death), Unique ID Assignment, Indication for CRID Assignment, and two disease specific inserts (Pre- and Post-HSCT Hodgkin and Non-Hodgkins Lymphoma).
    - The data from four recipient outcome forms were combined into new revisions of existing forms. AGNIS supported this change, so while there is a fewer number of forms the amount of data collected is still the same.
  - Started developing 4 cellular therapy forms that will be supported by AGNIS in 2018

- System Users:
  - Independent Transplant Centers:
    - 5 centers actively submitting and retrieving data through AGNIS: H. Lee Moffitt, MD Anderson, Cleveland Clinic, Stanford, and Maisonneuve-Rosemont Hospital
    - 2 center actively retrieving through AGNIS: Seidman Cancer Center and MD Anderson
  - Transplant centers using Vendor solutions:

- Eight vendor solutions supporting seventeen actively submitting centers and twenty-five retrieving centers
- Liaison Technologies: One site submitting data
- Management Science Associates: Three site submitting data
- Mediware: Two sites submitting data
- OTTR: Seven sites retrieving data
- StemSoft: One site submitting data
- StemTrek: One site submitting data
- Jagriti: One site submitting data
- Moffitt: One site submitting data (both a center and a vendor)
- Velos: Six sites retrieving
- TeleResults and Title21: authorized but not currently supporting centers

- System Enhancements:

In the last year, the AGNIS team accomplished the following:

- The AGNIS platform was used for over 26,000 submissions to FormsNet
- Provided ongoing support for EBMT-CIBMTR and CIBMTR-Eurocord AGNIS connections
- Released the new revisions of the 2400r5 Pre-Transplant Essential Data Form, 2402r1 Pre-Transplant Essential Data: Disease Classification Form, 2450r4 Post TED Form, 2100r4 100 Day Post-HSCT Data Form, 2005 HLA Form and 2900 Death Form

- Registry connections:
  - EBMT has been working with the CIBMTR to develop a pathway to share TED-level data from EBMT centers that also participate in the CIBMTR. Mapping has occurred for the Pre-TED, Post-TED at 100 days, Unique ID, and Infusion forms. Data submission, initially manually and now with automation for prospective data submitted for over 54 participating centers so far and plans continue to grow users
    - 8 centers with authorization to randomization to TED or CRF
    - 39 TED only centers
  - Received >73,000 forms in complete status from EBMT through the AGNIS submission process since the beginning of this project and over 30,000 in 2016

- Electronic Medical Records (EMR) connections:
  - CIBMTR worked with EPIC to integrate 51 standard CDEs into the BMT registration form in EPIC (BMT smartform).
    - Consists of HCT physicians and IT staff who are working to standardize data collection in the EMR to facilitate ease of data collection, consistent with national data standards, and submission for use of research

- Working with one EMR vendor (Epic) on development of data collection tools for the EMR that will use CIBMTR-defined data standards in the Cancer Data Standards Registry and Repository (caDSR) and Biomedical Research Integrated Domain Group (BRIDG); this project should serve to increase future interoperability of EMR systems with CIBMTR
- Developed three tools so far: aGVHD documentation flow sheet, cGVHD documentation tool, and BMT SmartForm

Information Management

The CIBMTR Information Management Strategy (IMS) project's main objective is to establish a comprehensive program for the management of data across the enterprise, turning the large volumes of data into a strategic asset supporting high value, sophisticated analyses. The Integrated Data Warehouse is the primary deliverable for this project. At delivery, the Integrated Data Warehouse will contain high quality, validated data readily available to researchers for immunobiology, outcomes, and other types of analyses. It will be the single source of truth of data that supports the diverse administrative and scientific needs of internal and external stakeholders. The team is building a unified domain to house multiple sources and dimensions of data. CIBMTR operational teams will be able to dramatically reduce the amount of time they spend on data consolidation, preparation, and validation of datasets and instead focus on the analysis. As a result, analyses will be completed in a timely manner facilitating decision-making based on these data assets.

- This effort is aligned with NMDP enterprise architectural standards, and incorporates selective use of industry standards, including BRIDG (Biomedical Research Integrated Domain Group) and HL-7 FHIR (Fast Healthcare Interoperability Resources).The first deliverable implemented an Integrated Data Store (IDS) which serves as the foundation for the long-term data warehouse. Using the IDS as the unified data source, the first phase of the Data Warehouse was completed by integrating data used for immunobiology analyses into the Data Warehouse. In FY17, the team completed the redesign of the architecture to more optimally support consolidation of data from various application sources as well as data and information provisioning to CIBMTR stakeholders, supporting future initiatives for faster, more flexible access to data. Accomplishments include: completion of the database design for the data warehouse, successful implementation of the physical model, including completion of loading a subset of CIBMTR data into the unified domain, proof of concept data extraction, and validation of the unified domain data extract against an existing comparable CIBMTR data set.

- As part of building the overall unified domain model, other accomplishments include:

- Designing an Extract Transfer Load (ETL) process and translation scripts for loading data from the data sources into the unified domain.
- Began initial design for analytical extract model.
- Completed metadata mapping for proof of concept data.
- Developed roadmap for future data population and extract capabilities.

Table 8 below shows the types of data stored in the Data Warehouse and their data sources, including data sources added since the original release of the IDS:

Table 8. Types of sources of data in CIBMTR Data Warehouse

Focus area	Description	Source
IDM	• Donor IDMs information for NMDP facilitated HCTs	Legacy (Formsnet1) & current FormsNet3
Infusion data	• 180 most Requested Variables for ad-hoc and center volumes reporting requests from FN3 • Clinical outcome data tied to each infusion event (future)	FormsNet, SIP
NMDP Source Data	• Cord Blood Unit Data • Double Cord (Multi)	StarLink CordLink (SyBase) CordSource through Reg ODS Emtrax through Reg ODS

Focus area	Description	Source
HLA/KIR Match Data	• Transformed CIBMTR Legacy HLA data • HLA data for donor/recipient for NMDP facilitated HCTs, legacy and current (STAR/SIP) (form 2005) • HLA data transformation on new form 2005/non-NMDP Tx SCTOD data • Donor-Recipient Match Grade results (HLA Save) • KIR data • Re-Evaluate current data sources	• CIBMTR OBS DB • STAR • FormsNet3 • IPR • HLA Save
Donor & Recipient Data	• Transformed Donor and Recipient data • Provides self-service environment for analysis through pre-defined joins (business view of the metadata), calculations and generating adhoc data sets • Capability for near real time(~ 5 minutes) data sharing and analytics across forms through combined and unified virtualization layer (views) • Faster turnaround on visibility to data quality fixes.	• FormsNet • NMDP Legacy
Metadata	• Provides data lineage, impact analysis and FormsNet metadata analysis	• FormsNet Metadata, BODI metadata, OBIEE metadata
Center volumes	• Provides metrics around the number of infusions by center/donor type/product type/disease/age group/race variables • Replaces existing manual process	• FormsNet, NMDP

Focus area	Description	Source
Repository Sample Data	• Integration with 3rd party vendor, Labvantage, to provide Research Sample data • Provides self-service environment for analysis through Business Intelligence tool. (OBIEE) • Provides end user defined reports utilized to complete HRSA reporting requirements.	• FormsNet, Labvantage
IDM	• Donor IDMs information for NMDP facilitated HCTs	Legacy (Formsnet1) & current FormsNet3
Clinical Trials **CT Rave**	• Integration with 3rd party vendor, Metadata Rave, to provide Clinical Trials data • Provides self-service environment for analysis through Business Intelligence tool. (OBIEE)	• Rave, NMDP, FormsNet
Audit	• Provide Business Intelligence environment (OBIEE) for internal Audit staff. • Provides end user defined reports and ad hoc analysis capabilities	• FormsNet3
Cellular Therapy	• Storage of Cellular Therapy data collected FormsNet3 forms	• FormsNet3

In addition to the referenced source data consolidated in the Data Warehouse, CIT has also implemented operational improvements to the warehouse, and developed, in the last 12 months, the following functionality:

- Data Quality Initiative: Data quality reporting dashboard has been developed and quality reports have been completed. Operational data quality checks and reports have been made available, allowing for early detection of questionable data in an effort to proactively identify and correct discrepant data, thus reducing the time spent preparing datasets
- Completed Data Warehouse Operational Improvements, including upgrades to the latest version of development tools and completion of automation of the Center Volumes Reporting Dashboard Data and Monthly Cord Blood Reports
- Enhancing the Business Intelligence application suite which shares data back with centers
    - Enhanced Data Back to Centers (eDBtC), which enables visualization of center trends and descriptive statistics as well as ad hoc querying capabilities,

was enhanced with an extension to include the addition of 25 data dimensions and filters to enable development of ad hoc queries, as well as new functionality and data for visualization of sub-disease and GVHD prophylaxis.
  - Center Performance Analytics (CPA), which enables a center to analyze center trends related to other centers in data set, create selective queries, and export filtered data for analysis, was accessed 466 times by 93 unique center users.
  - Rolled out ASBMT for RFI (Request for Information) report, which Streamlines preparation of center's ASBMT Annual Request for Information – Outcomes Data Form. Since its launch, we estimate that Data for RFI represent approximately 328 distinct sessions and 43 unique users of those transplant centers accessing the eDBtC application. Additionally, we have received positive feedback from centers who have expressed that Data for RFI has simplified their ASBMT RFI reporting process.

- We extended the daily LabVantage data feed to the Integrated Data warehouse by bringing in additional variables. We also created an Adhoc reporting environment, enabling business users to obtain faster access to data by creating their own reports.

- Updated the regular data feed from the Clinical Trials software, Medidata Rave, to the Integrated Data Warehouse by including additional variables. We also created an Adhoc reporting environment, enabling business users to create their own reports and thereby obtain faster access to data.

- Completed a Survivorship report. This is report is distributed on a weekly basis to Donor Centers to help track Survivor information. This report also eliminates dependency of legacy FormsNet form data to produce this report.

VI. Publications

1. Hashmi SK, Bredeson C, Duarte RF, et al. National Institutes of Health Blood and Marrow Transplant Late Effects Initiative: The Healthcare Delivery Working Group Report. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2017 May 1; 23(5):717-725. doi:10.1016/j.bbmt.2016.09.025. Epub 2016 Oct 3. PMC5378687.

2. Martin PJ, Fan W, Storer BE, et al. Replication of associations between genetic polymorphisms and chronic graft-versus-host disease. Blood. 2016 Nov 17; 128(20):2450-2456. doi:10.1182/blood-2016-07-728063. Epub 2016 Oct 6. PMC5114491.

3. Vierra-Green C, Roe D, Jayaraman J, et al. Estimating KIR haplotype frequencies on a cohort of 10,000 individuals: A comprehensive study on population variations, typing

resolutions, and reference haplotypes. PLoS One. 11(10):e0163973. doi:10.1371/journal.pone.0163973. Epub 2016 Oct 10. PMC5056762.

4. Wingard JR, Wood WA, Martens M, et al. Pretransplantation exercise and hematopoietic cell transplantation survival: A secondary analysis of Blood and Marrow Transplant Clinical Trials Network (BMT CTN 0902). Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2017 Jan 1; 23(1):161-164. doi:10.1016/j.bbmt.2016.10.007. Epub 2016 Oct 11. PMC5182134.

5. Hoff GA, Fischer JC, Hsu K, et al. Recipient HLA-C haplotypes and microRNA 148a/b binding sites have no impact on allogeneic hematopoietic cell transplantation outcomes. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2017 Jan 1; 23(1):153-160. doi:10.1016/j.bbmt.2016.09.028. Epub 2016 Oct 13. PMC5198579.

6. Switzer GE, Bruce J, Kiefer DM, et al. Health-related quality of life among older related hematopoietic stem cell donors (>60 years) is equivalent to that of younger related donors (18 to 60 years): A related donor safety study. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2017 Jan 1; 23(1):165-171. doi:10.1016/j.bbmt.2016.10.008. Epub 2016 Oct 14. PMC5182103.

7. Cornell RF, Bachanova V, D'Souza A, et al. Allogeneic transplantation for relapsed Waldenström macroglobulinemia and lymphoplasmacytic lymphoma. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2017 Jan 1; 23(1):60-66. doi:10.1016/j.bbmt.2016.10.010. Epub 2016 Oct 24. PMC5182098.

8. Abu Zaid M, Wu J, Wu C, et al. Plasma biomarkers of risk for death in a multicenter phase 3 trial with uniform transplant characteristics post-allogeneic HCT. Blood. 2017 Jan 12; 129(2):162-170. doi:10.1182/blood-2016-08-735324. Epub 2016 Nov 3. PMC5234220.

9. Rosko AE, Wang H-L, de Lima M, et al. Reduced intensity conditioned allograft yields favorable survival for older adults with B-cell acute lymphoblastic leukemia. American Journal of Hematology. 2017 Jan 1; 92(1):42-49. doi:10.1002/ajh.24575. Epub 2016 Nov 12. PMC5167625.

10. Cornell RF, D'Souza A, Kassim AA, et al. Maintenance versus induction therapy choice on outcomes after autologous transplantation for multiple myeloma. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow

Transplantation. 2017 Feb 1; 23(2):269-277. doi:10.1016/j.bbmt.2016.11.011. Epub 2016 Nov 15. PMC5346183.

11. Syrjala KL, Sutton SK, Jim HS, et al. Cancer and treatment distress psychometric evaluation over time: A BMT CTN 0902 secondary analysis. Cancer. 2017 Apr 15; 123(8):1416-1423. doi:10.1002/cncr.30454. Epub 2016 Nov 28. PMC5384862.

12. Chen Y-B, Wang T, Hemmer MT, et al. GVHD after umbilical cord blood transplantation for acute leukemia: an analysis of risk factors and effect on outcomes. Bone Marrow Transplantation. 2017 Mar 1; 52(3):400-408. doi:10.1038/bmt.2016.255. Epub 2016 Dec 12. PMC5332289.

13. Gluckman E, Cappelli B, Bernaudin F, et al. Sickle cell disease: An international survey of results of HLA-identical sibling hematopoietic stem cell transplantation. Blood. 2017 Mar 16; 129(11):1548-1556. doi:10.1182/blood-2016-10-745711. Epub 2016 Dec 13. PMC5356458.

14. Askar M, Sobecks R, Wang T, et al. MHC class I chain-related gene A (MICA) donor-recipient mismatches and MICA-129 polymorphism in unrelated donor hematopoietic cell transplantations has no impact on outcomes in acute lymphoblastic leukemia, acute myeloid leukemia, or myelodysplastic syndrome: A Center for International Blood and Marrow Transplant Research study. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2017 Mar 1; 23(3):436-444. doi:10.1016/j.bbmt.2016.11.021. Epub 2016 Dec 14. PMC5370205.

15. Hou L, Vierra-Green C, Lazaro A, et al. Limited HLA sequence variation outside of antigen recognition domain exons of 360 10 of 10 matched unrelated hematopoietic stem cell transplant donor-recipient pairs. HLA. 2017 Jan 1; 89(1):39-46. doi:10.1111/tan.12942. Epub 2016 Dec 15. PMC5425813.

16. Maziarz RT, Brazauskas R, Chen M, et al. Pre-existing invasive fungal infection is not a contraindication for allogeneic HSCT for patients with hematologic malignancies: a CIBMTR study. Bone Marrow Transplantation. 2017 Feb 1; 52(2):270-278. doi:10.1038/bmt.2016.259. Epub 2016 Dec 19. PMC5358320.

17. Ravandi F, Othus M, O'Brien S, et al. US intergroup study of chemotherapy plus dasatinib and allogeneic stem cell transplant in Philadelphia chromosome positive ALL Blood Advances. 1(3):250-259. doi:10.1182/bloodadvances.2016001495. Epub 2016 Dec 27.

18. Zheng C, Dai R, Hari PN, et al. Instrumental variable with competing risk model. Statistics in Medicine. 2017 Apr 15; 36(8):1240-1255. doi:10.1002/sim.7205. Epub 2017

Jan 8. PMC5479873.

19. El-Jawahri A, Chen Y-B, Brazauskas R, et al. Impact of pre-transplant depression on outcomes of allogeneic and autologous hematopoietic stem cell transplantation. Cancer. 2017 May 15; 123(10):1828-1838. doi:10.1002/cncr.30546. Epub 2017 Jan 19. PMC5419891.

20. Liu HD, Ahn KW, Hu Z-H, et al. Allogeneic hematopoietic cell transplant for adult chronic myelomonocytic leukemia. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. doi:10.1016/j.bbmt.2017.01.078. Epub 2017 Jan 20.

21. Michelis FV, Gupta V, Zhang M-J, et al. Cytogenetic risk determines outcomes after allogeneic transplantation in older patients with acute myeloid leukemia in their second complete remission: A Center for International Blood and Marrow Transplant Research cohort analysis. Cancer. 2017 Jun 1; 123(11):2035-2042. doi:10.1002/cncr.30567. Epub 2017 Jan 24. PMC5445018.

22. Weisdorf DJ, Millard HR, Horowitz MM, et al. Allogeneic transplantation for advanced acute myeloid leukemia: The value of complete remission. Cancer. 2017 Jun 1; 123(11):2025-2034. doi:10.1002/cncr.30536. Epub 2017 Jan 24. PMC5445001.

23. Ustun C, Giannotti F, Zhang M-J, et al. Outcomes of UCB transplantation are comparable in FLT3+ AML: Results of CIBMTR, eurocord and EBMT collaborative analysis. Leukemia. 2017 Jun 1; 31(6):1408-1414. doi:10.1038/leu.2017.42. Epub 2017 Jan 25. PMC5462854.

24. Brunstein C, Zhang M-J, Barker J, et al. The effect of inter-unit HLA matching in double umbilical cord blood transplantation for acute leukemia. Haematologica. doi:10.3324/haematol.2016.158584. Epub 2017 Jan 25.

25. Hamadani M, Kanate AS, DiGilio A, et al. Allogeneic hematopoietic cell transplantation for aggressive NK cell leukemia. A Center for International Blood and Marrow Transplant Research analysis. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2017 May 1; 23(5):853-856. doi:10.1016/j.bbmt.2017.01.082. Epub 2017 Feb 1. PMC5410937.

26. Lindsley RC, Saber W, Mar BG, et al. Prognostic mutations in myelodysplastic syndrome after stem-cell transplantation. New England Journal of Medicine. 2017 Feb 9; 376(6):536-547. doi:10.1056/NEJMoa1611604. Epub 2017 Feb 9. PMC5438571.

27. Scott BL, Pasquini MC, Logan BR, et al. Myeloablative vs. reduced intensity hematopoietic cell transplantation for acute myeloid leukemia and myelodysplastic syndromes. Journal of Clinical Oncology. 2017 Apr 10; 35(11):1154-1161. doi:10.1200/JCO.2016.70.7091. Epub 2017 Feb 13. PMC5455603.

28. Kamoun M, McCullough KP, Maiers M, et al. HLA amino acid polymorphisms and kidney allograft survival. Transplantation. 101(5):e170-e177. doi:10.1097/TP.0000000000001670. Epub 2017 Feb 18. NA.

29. Muraro PA, Pasquini M, Atkins HL, et al. Long-term outcomes after autologous hematopoietic stem cell transplantation for multiple sclerosis. JAMA Neurology. doi:10.1001/jamaneurol.2016.5867. Epub 2017 Feb 20.

30. Preussler JM, Meyer CL, Mau L-W, et al. Healthcare costs and utilization for patients age 50-64 years with acute myeloid leukemia treated with chemotherapy or with chemotherapy and allogeneic hematopoietic cell transplantation Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. doi:10.1016/j.bbmt.2017.02.017. Epub 2017 Mar 2.

31. Madbouly A, Wang T, Haagenson M, et al. Investigating the association of genetic admixture and donor/recipient genetic disparity with transplant outcomes. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. doi:10.1016/j.bbmt.2017.02.019. Epub 2017 Mar 2.

32. Garderet L, D'Souza A, Jacobs P, et al. Response assessment in myeloma: practical manual on consistent reporting in an era of dramatic therapeutic advances. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2017 Jul 1; 23(7):1193-1202. doi:10.1016/j.bbmt.2017.03.009. Epub 2017 Mar 8. NA.

33. Gerds AT, Woo Ahn K, Hu ZH, et al. Outcomes after umbilical cord blood transplantation for myelodysplastic syndromes. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2017 Jun 1; 23(6):971-979. doi:10.1016/j.bbmt.2017.03.014. Epub 2017 Mar 10. PMC5474679.

34. Khoury HJ, Wang T, Hemmer MT, et al. Improved survival after acute graft vs. host disease diagnosis in the modern era. Haematologica. doi:10.3324/haematol.2016.156356. Epub 2017 Mar 16.

35. Kekre N, Zhang Y, Zhang M-J, et al. Effect of antithymocyte globulin source on outcomes of bone marrow transplantation for severe aplastic anemia. Haematologica.

doi:10.3324/haematol.2017.164459. Epub 2017 Mar 24.

36. Cheng YC, Shi Y, Zhang M-J, et al. Long-term outcome of inflammatory breast cancer compared to non-inflammatory breast cancer in the setting of high-dose chemotherapy with autologous hematopoietic cell transplantation. Journal of Cancer. 8(6):1009-1017. doi:10.7150/jca.16870. Epub 2017 Mar 25. PMC5436253.

37. Wang Y, Wang T, Dagnall C, et al. Relative telomere length prior to hematopoietic cell transplantation (HCT) and outcome after unrelated donor HCT for acute leukemia. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. doi:DOI: 10.1016/j.bbmt.2017.03.032. Epub 2017 Apr 4.

38. Slack J, Albert MH, Balashov D, et al. Outcome of hematopoietic cell transplantation for DNA-double strand breakage repair disorders. Journal of Allergy and Clinical Immunology. doi:10.1016/j.jaci.2017.02.036. Epub 2017 Apr 7.

39. Halagan M, Manor S, Shriki N, et al. East meets west - impact of ethnicity on donor match rates in the Ezer Mizion Bone Marrow Donor Registry. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. doi:10.1016/j.bbmt.2017.04.005. Epub 2017 Apr 7. NA.

40. Gabriel M, Shaw B, Brazauskas R, Chen M, Margolis DA, Sengelov H, Dahlberg A, Ahmed IA, Delgado D, Lazarus HM, Gibson B, Myers KC, Kamble RT, Abdel-Mageed A, Li C-K, Flowers MED, Battiwalla M, Savani BN, Majhail N, Shaw P. Risk factors for subsequent central nervous system tumors in pediatric allogeneic hematopoietic cell transplant: A study from the Center for International Blood and Marrow Transplant Research. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. doi:10.1016/j.bbmt.2017.04.004. Epub 2017 Apr 12.

41. Khandelwal P, Millard HR, Thiel E, et al. Hematopoietic stem cell transplant activity in pediatric cancer between 2008 and 2014 in the United States: a CIBMTR report. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. doi:10.1016/j.bbmt.2017.04.018. Epub 2017 Apr 24.

42. Pappas DJ, Lizee A, Paunic V, et al. Significant variation between SNP-based HLA imputations in diverse populations: the last mile is the hardest. The Pharmacogenomics Journal. doi:10.1038/tpj.2017.7. Epub 2017 Apr 25.

43. Segal E, Martens M, Wang HL, et al. Comparing outcomes of matched related donor and matched unrelated donor hematopoietic cell transplants in adults with B-Cell acute

lymphoblastic leukemia. Cancer. doi:10.1002/cncr.30737. Epub 2017 Apr 27.

44. Vrooman LM, Millard HR, Brazauskas R, et al. Survival and late effects after allogeneic hematopoietic cell transplantation for hematologic malignancy at less than three years of age. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. doi:10.1016/j.bbmt.2017.04.017. Epub 2017 Apr 28.

45. Krakow EF, Hemmer M, Wang T, et al. Tools for the precision medicine era: How to develop highly personalized treatment recommendations from cohort and registry data using Q-learning. American Journal of Epidemiology. doi:10.1093/aje/kwx027. Epub 2017 May 3.

46. Schriber JR, Hari PN, Ahn KW, et al. Hispanics have the lowest stem cell transplant utilization rate for autologous hematopoietic cell transplantation for multiple myeloma in the United States: A CIBMTR report. Cancer. doi:10.1002/cncr.30747z. Epub 2017 May 4.

47. Boudreau JE, Giglio F, Gooley TA, et al. KIR3DL1/HLA-B subtypes govern acute myelogenous leukemia relapse after hematopoietic cell transplantation. Journal of Clinical Oncology. doi:10.1200/JCO.2016.70.7059. Epub 2017 May 18.

48. Roe D, Vierra-Green C, Pyo C-W, et al. Revealing complete complex KIR haplotypes phased by long-read sequencing technology. Genes and Immunity. doi:10.1038/gene.2017.10. Epub 2017 Jun 1. NA.

49. Fleischhauer K, Ahn KW, Wang HL, et al. Directionality of non-permissive HLA-DPB1 T-cell epitope group mismatches does not improve clinical risk stratification in 8/8 matched unrelated donor hematopoietic cell transplantation. Bone Marrow Transplantation. doi:10.1038/bmt.2017.96. Epub 2017 Jun 5.

50. D'Souza A, Lee S, Zhu X, Pasquini M. Current use and trends in hematopoietic cell transplantation in the United States. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. doi:10.1016/j.bbmt.2017.05.035. Epub 2017 Jun 9.

51. Epperla N, Ahn KW, Ahmed S, et al. Rituximab-containing reduced-intensity conditioning improves progression-free survival following allogeneic transplantation in B cell non-Hodgkin lymphoma. Journal of Hematology & Oncology. doi:10.1186/s13045-017-0487-y. Epub 2017 Jun 12.

52. Eapen M, Wang T, Veys PA, et al. Allele-level HLA matching for umbilical cord blood transplantation for non-malignant diseases in children: a retrospective analysis. The

Lancet Haematology. doi:10.1016/S2352-3026(17)30104-7. Epub 2017 Jun 13.

53. Bashey A, Zhang M-J, McCurdy SR, et al. Mobilized peripheral blood stem cells versus unstimulated bone marrow as a graft source for T-cell?replete haploidentical donor transplantation using post-transplant cyclophosphamide. Journal of Clinical Oncology. doi:10.1200/JCO.2017.72.8428. Epub 2017 Jun 23.

54. Switzer GE, Bruce J, Pastorek G, et al. Parent versus Child Donor Perceptions of the Bone Marrow Donation Experience. Bone Marrow Transplantation. doi:10.1038/bmt.2017.124. Epub 2017 Jun 26.

55. Eapen M, Kurtzberg J, Zhang MJ, et al. Umbilical cord blood transplantation in children with acute leukemia: Impact of conditioning on transplantation outcomes. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2017 Oct 2; 23(10):1714-1721. doi:10.1016/j.bbmt.2017.06.023. Epub 2017 Jul 3. PMC5605440.

56. Muffly L, Pasquini M, Martens M, et al. Increasing use of allogeneic hematopoietic cell transplantation in patients aged 70 years and older in the United States. Blood. 2017 Aug 31; 130(9):1156-1164. doi:10.1182/blood-2017-03-772368. Epub 2017 Jul 3. PMC5580273.

57. Xie C, Yeo ZX, Wong M, et al. Fast and accurate HLA typing from short-read next-generation sequence data with xHLA. Proceedings of the National Academy of Sciences of the United States of America. 2017 Jul 3; 114(30):8059-8064. doi:10.1073/pnas.1707945114. Epub 2017 Jul 3. PMC5544337.

58. Kanate AS, DiGilio A, Ahn KW, et al. Allogeneic haematopoietic cell transplantation for extranodal natural killer/T-cell lymphoma, nasal type: A CIBMTR analysis. British Journal of Haematology. doi:10.1111/bjh.14879. Epub 2017 Aug 2. PMC5796874.

59. Ahn KW, Banerjee A, Sahr N, et al. Group and within-group variable selection for competing risks data. Lifetime Data Analysis. doi:10.1007/s10985-017-9400-9 Epub 2017 Aug 4. PMC5797529.

60. Karaesmen E, Rizvi AA, Preus LM, et al. Replication and validation of genetic polymorphisms associated with survival after allogeneic blood or marrow transplant. Blood. 2017 Sep 28; 130(13):1585-1596. doi:10.1182/blood-2017-05-784637. Epub 2017 Aug 15. PMC5620418.

61. Shaw BE, Brazauskas R, Millard HR, et al. Centralized patient-reported outcome data collection in transplantation is feasible and clinically meaningful. Cancer. 2017 Dec 1;

123(23):4687-4700. doi:10.1002/cncr.30936. Epub 2017 Aug 17. PMC5693638.

62. Arnold SD, Brazauskas R, He N, et al. Clinical risks and healthcare utilization of haematopoietic cell transplantation for sickle cell disease in the U.S. using merged databases. Haematologica. 2017 Nov 1; 102(11):1823-1832. doi:10.3324/haematol.2017.169581. Epub 2017 Aug 17. PMC5664386.

63. Holstein SA, Jung S-H, Richardson PG, et al. Updated analysis of CALGB (Alliance) 100104 assessing lenalidomide versus placebo maintenance after single autologous stem-cell transplantation for multiple myeloma: a randomised, double-blind, phase 3 trial. The Lancet Haematology. 2017 Sep 1; 4(9):e431-e442. doi:10.1016/S2352-3026(17)30140-0. Epub 2017 Aug 17. PMC5718627.

64. Alter I, Gragert L, Fingerson S, et al. HLA class I haplotype diversity is consistent with selection for frequent existing haplotypes. PLOS Computational Biology. 13(8):e1005693. doi:10.1371/journal.pcbi.1005693. Epub 2017 Aug 28. PMC5590998.

65. Abraham A, Hsieh M, Eapen M, et al. Relationship between mixed donor-recipient chimerism and disease recurrence after hematopoietic cell transplantation for sickle cell disease. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2017 Dec 1; 23(12):2178-2183. doi:10.1016/j.bbmt.2017.08.038. Epub 2017 Sep 4. PMC5782809.

66. Malogolowkin MH, Hemmer MT, Le-Rademacher J, et al. Outcomes following autologous hematopoietic stem cell transplant for patients with relapsed Wilms' tumor: A CIBMTR retrospective analysis. Bone Marrow Transplantation. 2017 Nov 1; 52(11):1549-1555. doi:10.1038/bmt.2017.178. Epub 2017 Sep 4. PMC5665725.

67. Clay-Gilmour AI, Hahn T, Preus LM, et al. Genetic association with B-cell acute lymphoblastic leukemia in allogeneic transplant patients differs by age and sex. Blood Advances. 2017 Sep 12; 1(20):1717-1728. doi:10.1182/bloodadvances.2017006023. Epub 2017 Sep 8. PMC5728332.

68. Liu Y, Logan B, Liu N, et al. Deep reinforcement learning for dynamic treatment regimes on medical registry data. IEEE International Conference on Healthcare Informatics. 2017 Aug 23; 2017:380-385. doi:10.1109/ICHI.2017.45. Epub 2017 Sep 14. PMC5856473.

69. Mahindra A, Hari P, Fraser R, et al. Autologous hematopoietic cell transplantation for multiple myeloma patients with renal insufficiency: A Center for International Blood and Marrow Transplant Research analysis. Bone Marrow Transplantation. 2017 Dec 1; 52(12):1616-1622. doi:10.1038/bmt.2017.198. Epub 2017 Sep 18. PMC5859934.

70. Kelly DL, Buchbinder D, Duarte RF, et al. Neurocognitive dysfunction in hematopoietic cell transplant recipients: Expert review from the Late Effects and Quality of Life Working Committee of the Center for International Blood and Marrow Transplant Research and Complications and Quality of Life Working Party of the European Society for Blood and Marrow Transplantation. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2018 Feb 1; 24(2):228-241. doi:10.1016/j.bbmt.2017.09.004. Epub 2017 Sep 20. PMC5768142.

71. Stroncek DF, Shaw BE, Logan BR, et al. Donor experiences of second marrow or peripheral blood stem cell collection mirror the first, but CD34+ yields are less. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2018 Jan 1; 24(1):175-184. doi:10.1016/j.bbmt.2017.09.013. Epub 2017 Sep 25. PMC5743544.

72. Heimall J, Logan BR, Cowan MJ, et al. Immune reconstitution and survival of 100 SCID patients post-hematopoietic cell transplant: A PIDTC natural history study. Blood. 2017 Dec 21; 130(25):2718-2727. doi:10.1182/blood-2017-05-781849. Epub 2017 Oct 11. PMC5746165.

73. Hill BT, Ahn KW, Hu Z-H, et al. Assessment of impact of HLA type on outcomes of allogeneic hematopoietic stem cell transplantation for chronic lymphocytic leukemia. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2018 Mar 1; 24(3):581-586. doi:10.1016/j.bbmt.2017.10.015. Epub 2017 Oct 12. PMC5944847.

74. Epperla N, Ahn KW, Armand P, et al. Fludarabine and busulfan versus fludarabine, cyclophosphamide, and rituximab as reduced-intensity conditioning for allogeneic transplantation in follicular lymphoma. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2018 Jan 1; 24(1):78-85. doi:10.1016/j.bbmt.2017.10.011. Epub 2017 Oct 13. PMC5743624.

75. Turcotte LM, DeFor TE, Newell LF, et al. Donor and recipient plasma follistatin levels are associated with acute GvHD in Blood and Marrow Transplant Clinical Trials Network 0402. Bone Marrow Transplantation. 2018 Jan 1; 53(1):64-68. doi:10.1038/bmt.2017.236. Epub 2017 Oct 23. PMC5752567.

76. Htut M, D'Souza A, Krishnan A, et al. Autologous/allogeneic Hematopoietic cell transplantation versus tandem autologous transplantation for multiple myeloma: Comparison of long-term postrelapse survival. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2018 Mar 1; 24(3):478-485. doi:10.1016/j.bbmt.2017.10.024. Epub 2017 Oct 24.

PMC5826888.

77. Shaw BE, Syrjala KL, Onstad LE, et al. PROMIS measures can be used to assess symptoms and function in long-term hematopoietic cell transplantation survivors. Cancer. 2018 Feb 15; 124(4):841-849. doi:10.1002/cncr.31089. Epub 2017 Oct 26. PMC5800994.

78. Louzoun Y, Alter I, Gragert L, et al. Modeling coverage gaps in haplotype frequencies via Bayesian inference to improve stem cell donor selection. Immunogenetics. doi:10.1007/s00251-017-1040-4. Epub 2017 Nov 9. NA.

79. Myers RM, Hill BT, Shaw BE, et al. Long-term outcomes among 2-year survivors of autologous hematopoietic cell transplantation for Hodgkin and diffuse large b-cell lymphoma. Cancer. 2018 Feb 15; 124(4):816-825. doi:10.1002/cncr.31114. Epub 2017 Nov 10. PMCID5871233.

80. Kumar SK, Dispenzieri A, Fraser R, et al. Early relapse after autologous hematopoietic cell transplantation remains a poor prognostic factor in multiple myeloma but outcomes have improved over time. Leukemia. 2018 Apr 1; 32(4):986-995. doi:10.1038/leu.2017.331. Epub 2017 Nov 16. PMC5871538.

81. William BM, Wang T, Haagenson MD, et al. Impact of HLA alleles on outcomes of allogeneic transplantation for B cell non-Hodgkin lymphomas: A Center for International Blood And Marrow Transplant Research analysis. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2018 Apr 1; 24(4):827-831. doi:10.1016/j.bbmt.2017.11.003. Epub 2017 Nov 16. PMC5902644.

82. Qayed M, Wang T, Hemmer MT, et al. Influence of age on acute and chronic GVHD in children undergoing HLA-identical sibling bone marrow transplantation for acute leukemia: Implications for prophylaxis. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2018 Mar 1; 24(3):521-528. doi:10.1016/j.bbmt.2017.11.004. Epub 2017 Nov 16. PMC5826854.

83. Hamadani M, Horowitz MM. Allogeneic transplantation for follicular lymphoma: Does one size fit all? Journal of Oncology Practice. 2017 Dec 1; 13(12):798-806. doi:10.1200/JOP.2017.026336. Epub 2017 Dec 1. PMC5728364.

84. Kebriaei P, Anasetti C, Zhang M-J, et al. Intravenous busulfan compared with total body irradiation pretransplant conditioning for adults with acute lymphoblastic leukemia. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2018 Apr 1; 24(4):726-733.

doi:10.1016/j.bbmt.2017.11.025. Epub 2017 Dec 2. PMC5902420.

85. Neumann JL, Mau L-W, Virani S, et al. Burnout, Moral Distress, Work-Life Balance and Career Satisfaction among Hematopoietic Cell Transplantation Professionals Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. doi:10.1016/j.bbmt.2017.11.015. Epub 2017 Dec 2. NA.

86. Casulo C, Friedberg JW, Ahn KW, et al. Autologous transplantation in follicular lymphoma with early therapy failure: A National LymphoCare Study and Center for International Blood and Marrow Transplant Research analysis. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2018 Jun 1; 24(6):1163-1171. doi:10.1016/j.bbmt.2017.12.771. Epub 2017 Dec 11. PMC5993598.

87. Holstein SA, Avet-Loiseau H, Hahn T, et al. BMT CTN Myeloma Intergroup Workshop on minimal residual disease and immune profiling: Summary and recommendations from the organizing committee. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2018 Apr 1; 24(4):641-648. doi:10.1016/j.bbmt.2017.12.774. Epub 2017 Dec 11. PMC5902638.

88. Chang C-J, Osoegawa K, Milius RP, et al. Collection and storage of HLA NGS genotyping data for the 17th International HLA and Immunogenetics Workshop. Human Immunology. doi:10.1016/j.humimm.2017.12.004. Epub 2017 Dec 14. PMC5805642.

89. Logan BR, Sparapani R, McCulloch RE, et al. Decision making and uncertainty quantification for individualized treatments using Bayesian Additive Regression Trees. Statistical Methods in Medical Research. doi:10.1177/0962280217746191. Epub 2017 Dec 18.

90. Bejanyan N, Zhang M-J, Wang H-L, et al. Pretransplant consolidation is not beneficial for adults with ALL undergoing myeloablative allogeneic transplantation. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2018 May 1; 24(5):945-955. doi:10.1016/j.bbmt.2017.12.784. Epub 2017 Dec 21. PMC5953798.

91. Gadalla SM, Wang T, Loftus D, et al. No association between donor telomere length and outcomes after allogeneic unrelated hematopoietic cell transplant in patients with acute leukemia. Bone Marrow Transplantation. 2018 Apr 1; 53(4):383-391. doi:10.1038/s41409-017-0029-9. Epub 2017 Dec 21. PMC5898974.

92. Jones RB, Martinez C, Majhail NS, et al. Stem cell transplantation and informatics - current considerations. Biology of Blood and Marrow Transplantation: Journal of the

American Society for Blood and Marrow Transplantation. doi:10.1016/j.bbmt.2017.12.792. Epub 2017 Dec 27. NA.

93. Smith EP, Li H, Friedberg JW, et al. Tandem autologous hematopoietic cell transplantation for patients with primary progressive or recurrent Hodgkin lymphoma: A SWOG and Blood and Marrow Transplant Clinical Trials Network phase II trial (SWOG S0410/BMT CTN 0703). Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2018 Apr 1; 24(4):700-707. doi:10.1016/j.bbmt.2017.12.798. Epub 2017 Dec 28. PMC5965270.

94. Pasquini MC, Logan B, Jones RJ, et al. Blood and Marrow Transplant Clinical Trials Network report on development of novel endpoints and selection of promising approaches for graft-versus-host disease prevention trials. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2018 Jun 1; 24(6):1274-1280. doi:10.1016/j.bbmt.2018.01.002. Epub 2018 Jan 8. PMC5993573.

95. Hurley CK, Hou L, Lazaro A, et al. Next generation sequencing characterizes the extent of HLA diversity in an Argentinian registry population. HLA. doi:10.1111/tan.13210. Epub 2018 Jan 12. NA.

96. Buchbinder D, Kelly DL, Duarte RF, et al. Neurocognitive dysfunction in hematopoietic cell transplant recipients: Expert review from the Late Effects and Quality of Life Working Committee of the CIBMTR and Complications and Quality of Life Working Party of the EBMT. Bone Marrow Transplantation. 2018 May 1; 53(5):535-555. doi:10.1038/s41409-017-0055-7. Epub 2018 Jan 17. PMC5985976.

97. Lee C, Haneuse S, Wang H-L, et al. Prediction of acute graft-versus-host disease following hematopoietic cell transplantation. PLoS One. 13(1):e0190610. doi:10.1371/journal.pone.0190610. Epub 2018 Jan 18. PMC5773230.

98. Drobyski WR, Szabo A, Zhu F, et al. Tocilizumab, tacrolimus and methotrexate for the prevention of acute graft-versus-host disease: Low incidence of lower gastrointestinal tract disease. Haematologica. 2018 Apr 1; 103(4):717-727. doi:10.3324/haematol.2017.183434. Epub 2018 Jan 19. PMC5865423.

99. Turcotte LM, Wang T, Hemmer MT, et al. Donor body mass index does not predict graft versus host disease following hematopoietic cell transplantation. Bone Marrow Transplantation. doi:10.1038/s41409-018-0100-1. Epub 2018 Jan 30.

100. Buturovic L, Shelton J, Spellman SR, et al. Evaluation of a machine learning-based prognostic model for unrelated hematopoietic cell transplantation donor selection.

Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2018 Jun 1; 24(6):1299-1306. doi:10.1016/j.bbmt.2018.01.038. Epub 2018 Feb 1. PMC5993610.

101. Burns LJ, Abetti B, Arnold SD, et al. Engaging patients in setting a patient-centered outcomes research agenda in hematopoietic cell transplantation Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. doi:https://doi.org/10.1016/j.bbmt.2018.01.029. Epub 2018 Feb 2. N/A.

102. Roelen D, de Vaal Y, Vierra-Green C, et al. HLA mismatches that are identical for the antigen recognition domain are less immunogenic. Bone Marrow Transplantation. doi:10.1038/s41409-018-0108-6. Epub 2018 Feb 6. NA.

103. Sureda A, Zhang M-J, Dreger P, et al. Allogeneic hematopoietic stem cell transplantation for relapsed follicular lymphoma: A combined analysis on behalf of the Lymphoma Working Party of the EBMT and the Lymphoma Committee of the CIBMTR. Cancer. 2018 Apr 15; 124(8):1733-1742. doi:10.1002/cncr.31264. Epub 2018 Feb 9. PMC5946312.

104. McCurdy SR, Zhang M-J, St Martin A, et al. Effect of donor characteristics on haploidentical transplantation with posttransplantation cyclophosphamide. Blood Advances. 2018 Feb 13; 2(3):299-307. doi:10.1182/bloodadvances.2017014829. Epub 2018 Feb 9. PMC5812334.

105. Shaw BE, Logan BR, Spellman SR, et al. Development of an unrelated donor selection score predictive of survival after HCT: Donor age matters most. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. 2018 May 1; 24(5):1049-1056. doi:10.1016/j.bbmt.2018.02.006. Epub 2018 Feb 14. PMC5953795.

106. Andermann T, Peled J, Ho C, et al. Microbiome-host interactions in hematopoietic stem-cell transplant recipients. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. doi:10.1016/j.bbmt.2018.02.009. Epub 2018 Feb 19.

107. Ahn KW, Kim S. Variable selection with group structure in competing risks quantile regression. Statistics in Medicine. 2018 Apr 30; 37(9):1577-1586. doi:10.1002/sim.7619. Epub 2018 Feb 21. PMC5889760.

108. Stiff PJ, Montesinos P, Peled T, et al. Cohort-controlled comparison of umbilical cord blood transplantation using carlecortemcel-L, a single progenitor-enriched cord blood, to double cord blood unit transplantation. Biology of Blood and Marrow Transplantation:

Journal of the American Society for Blood and Marrow Transplantation. doi:10.1016/j.bbmt.2018.02.012. Epub 2018 Mar 1.

109. D'Souza A, Millard H, Knight J, et al. Prevalence of self-reported sleep dysfunction before allogeneic hematopoietic cell transplantation. Bone Marrow Transplantation. doi:10.1038/s41409-018-0150-4. Epub 2018 Mar 7.

110. Rashidi A, Shanley R, Yohe SL, et al. Association between recipient TNF rs361525 and acute GVHD: Results from analysis of BMT CTN-0201 samples. Bone Marrow Transplantation. doi:10.1038/s41409-018-0127-3. Epub 2018 Mar 7.

111. Jim HSL, Sutton S, Najhail NS et al. Severity, course, and predictors of sleep disrution following hematopoietic cell transplantation: A secondary data analysis from the BMT CTN 0902 trial Bone Marrow Transplantation. doi:10.1038/s41409-018-0138-0. Epub 2018 Mar 7.

112. Martens M, Logan BR. A Group Sequential Test for Treatment Effect based on the Fine-Gray Model. Biometrics. doi:10.1111/biom.12871. Epub 2018 Mar 13.

113. Wood WA, Brazauskas R, Hu ZH, et al. Country-level macroeconomic indicators predict early post-allogeneic hematopoietic cell transplantation survival in acute lymphoblastic leukemia: A CIBMTR analysis. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. doi:10.1016/j.bbmt.2018.03.016. Epub 2018 Mar 19.

114. Switzer GE, Macis M, Fabi R, et al. Providing level-of-match information to perfectly matched unrelated donors: Evaluating acceptability and potential changes in donor availability. Biology of Blood and Marrow Transplantation: Journal of the American Society for Blood and Marrow Transplantation. doi:10.1016/j.bbmt.2018.03.017. Epub 2018 Mar 21. NA.

115. Duncan CN, Brazauskas R, Huang J, et al. Late cardiovascular morbidity and mortality following pediatric allogeneic hematopoietic cell transplantation. Bone Marrow Transplantation. doi:10.1038/s41409-018-0155-z. Epub 2018 Mar 26.

VII. Abstracts

1. Bejanyan N, Weisdorf D, LazaryanA. Consolidation chemotherapy is not beneficial for adult acute lymphoblastic leukemia patients with available donor undergoing myeloablatice allogeneic hematopoietic cell transplantation in first complete remission: A

CIBMTR study. ASH 2016.

2. Kebriae P, Aldoss I. Comparison of total body irradiation-based with intravenous bulsulfan based chemotherapy only conditioning regimens for myeloablative hematopoietic transplantation (HCT) in adults with acute lymphoblastic leukemia. ASH 2016.

3. Hill B. Assessment of human leukocyte antigen (HLA) type on outcomes of allogeneic transplant for chronic lymphocytic leukemia (CLL). ASH 2016.

4. Stroncek D. Pain, symptoms, Aes and recovery after second unrelated donor collection of marrow/peripheral blood stem cells are similar to those of the first donation. ASH 2016.

5. Bashey A, Hamadani M. Comparison of peripheral blood stem cells (PBSC) to bone marrow (BM) for t-replete HLA-haploidentical donor transplantation using post-transplant cyclophosphamide. ASH 2016.

6. Kumar A, Loren A. Unrelated male donors versus sibling parous female donors: impact on transplant related outcomes. ASH 2016.

7. Qayed M, Horan J. Influence of age on risk for acute and chronic GVHD in children receiving HLA identical sibling bone marrow transplantation. ASH 2016.

8. Paulson K. Seftel M. Inferior access to allogeneic transplant in disadvantaged population: a CIBMTR analysis. ASH 2016.

9. Satwani P, Aplenc R. Role of donor source on clinical outcomes and inpatient resource utilization for hematopoietic cell transplantation in children with acute leukemia. ASH 2016.

10. Hahn T. Exome array analyses identify new genes influencing survival outcomes after HLA-matched unrelated donor blood and marrow transplantation. ASH 2016.

11. Hahn T. Replication of candidate SNP survival analyses and gene-based tests of association with survival outcomes after an unrelated donor blood or marrow transplant: results from the discovery-BMT study. ASH 2016.

12. Hahn T. Exome array analyses identify low-frequency germline variants associated with increased risk of AML in a HLA-matched unrelated donor blood and marrow transplant population. ASH 2016.

13. Gadalla S. Germline mutations in patients receiving unrelated donor hematopoietic cell transplant for severe aplastic anemia. ASH 2016.

14. Hill B. Impact of human leukocyte antigen (HLA) alleles on outcomes of allogeneic transplantation (AlloHCT) for b-cell non-hodgkin lymphomas (B-NHL); a CIBMTR analysis. ASH 2016.

15. Saber W. Pilot study of prognostic impact of pre-allogeneic hematopoietic cell transplantation (HCT) plasma levels of CXC-chemokines (CXCL-4 and CXCL-7) in patients with myelodysplastic syndromes (MDS). ASH 2016.

16. Saber W. Genetic alterations predict outcomes in patients with myelodysplastic syndrome receiving allogeneic hematopoietic stem cell transplantation. ASH 2016.

17. Gadalla S. Donor telomere length and outcomes after allogeneic unrelated hematopoietic cell transplant in patients with acute leukemia. ASH 2016.

18. Mahindra A. Patiens (pts) with Renal Insufficiency (RI) and multiple myeloma (MM) have similar outcomes after autologous hematopoietic cell transplantation (AHCT) as those without. ASH 2016.

19. Krishnan A, Sharma M. Survival after relapse following tandem allogeneic vs tandem autologous hematopoietic cell transplantation (HCT) for myeloma (MM). ASH 2016.

20. Schriber J. Significant differences in stem cell transplant utilization rates (STUR) of autologouse hematopoietic cell transplant (AHCT) in multiple myeloma (MM) based on ethnicity without differences in efficacy: a CIBMTR report. ASH 2016.

21. Levine J, Harris A. Comparision of outcomes of myeloablative conditioning regimens combining busulfan with either cyclophosphamide or fludarbine in children. ASH 2016.

22. Strouse C. Stratification of allogeneic hematopoietic cell transplant patients by risk of developing veno-occlusive disease: a model for assigning a high-risk score. ASH 2016.

23. Trends in pre and post transplant therapies prior to first autologous hematopoietic cell transplantation among patients with multiple myeloma in the United States, 2004-2014. ASH 2016.

24. Pagel J. Feasibility of Allogeneic Hematopoietic Cell Transplantation Among High-Risk AML Patients in First Complete Remission: Results of the Transplant Objective from the SWOG (S1203) Randomized Phase III Study of Induction Therapy Using Standard 7+3 Therapy or Idarubicin with High-Dose Cytarabine (IA) Versus IA Plus Vorinostat. ASH

2016.

25. Umbilical cord blood (UCB) transplantation in children with acute leukemia: impact of conditioning regimen on transplant outcomes. ASH 2016.

26. Holtan S. Follistatin and Endoglin: Potential Biomarkers of Endothelial Damage and Non-Relapse Mortality after Myeloablative Allogeneic Hematopoietic Cell Transplantation. ASH 2016.

27. Evaluation of Immune Recovery following Autologous Hematopoietic cell transplantation in HIV-related lymphoma: Results of the BMT CTN/AMC 07[illegible] Trial. ASH 2016.

28. Pasquini M. Comparison of Autologous Hematopoietic Cell Transplant (autoHCT), Bortezomib, Lenalidomide (Len) and Dexamethasone (RVD) Consolidation and Len Maintenance (ACM), Tandem autoHCT with Len Maintenance (TAM) and autoHCT with Len Maintenance (AM) for Up-Front Treatment of Patients with Multiple Myeloma (MM): Primary Results from the Randomized Phase 3 Trial of the Blood and Marrow Transplant Clinical Trials Network (BMT CTN 0702 – StaMINA Trial). ASH 2016.

29. Ustun C. Impact of early bloodstream infection (BSI) by vancomycin-resistant enterococci (VRE) on long-term transplant outcomes. Tandem 2017.

30. Wang Y. Recipient Pre-HCT telomere length and outcomes after unrelated donor HCT for acute leukemia. Tandem 2017.

31. Spierings E. Analysis of predicted indirectly recognizable HLA epitopes (PIRCHE) in mismatched unrelated donor hematopoietic stem cell transplants (HCT): a center for international blood and marrow transplant research (CIBMTR) cohort study. Tandem 2017.

32. Hashmi S, Dean R. Risks of New Myeloid Neoplasms after Autologous Transplant for Plasma Cell Myeloma and Lymphomas: Effects of Drug and Ionizing Radiation Exposures. Tandem 2017.

33. Satwani P. Long-term outcomes among two-year survivors of autologous hematopoietic cell transplant for hodgkin and diffuse large b-cell lymphoma. Tandem 2017.

34. Epperla N. Rituximab versus non-rituximab containing reduced intensity conditioning (RIC) regimens for allogeneic hematopoietic cell transplantation (alloHCT) in b-cell non-hodgkin lymphomas (B-NHL): A CIBMTR analysis. Tandem 2017.

35. Kanate A. Allogeneic hematopoietic cell transplantation (alloHCT) for extranodal natural killer (NK)/T-cell lymphoma, nasal type (ENKL): A CIBMTR analysis. Tandem 2017.

36. Casulo C, Friedberg J. Autologous transplantation (autoHCT) is associated with improved overall survival (OS) in follicular lymphoma patients (pts) experiencing early therapy failure after frontline chemo-immunotherapy: a national lymphocare study (NLCS) & CIBMTR analysis. Tandem 2017.

37. Dispenzier A, Kumar S. Trends in survival outcomes among patients (pts) relapsing early after autologous stem cell transplantation (ASCT) for multiple myeloma (MM). Tandem 2017.

38. Sabloff M. Impact of higher dose total body irradiation conditioning on outcome of an allogeneic hematopoietic cell transplant in the modern era. Tandem 2017.

39. Hahn T. Novel genetic variants associated with death due to acute lymphoblastic leukemia within one year after HLA-matched unrelated donor blood and marrow transplantation (DISCOVeRY-BMT study). Tandem 2017.

40. Sucheston-Campbell L. Functional genetic variants on 14q32 associate with death due to acute myeloid leukemia (AML) and myelodysplastic syndrome (MDS) within one year after HLA-matched unrelated donor blood and marrow transplantation (DISCOVeRY BMT Study). Tandem 2017.

41. Khera M. Understanding the physicians perspectives about translating research into clinical practice: example of blood and marrow transplant clinical trials network (BMT CTN) 0201 results. Tandem 2017.

42. Denzen E. Lessons learned from merging CIBMTR data and CMS medicare claims data. Tandem 2017.

43. Saber W. Stratification of allogeneic hematopoietic cell transplant patients by risk of developing veno-occlusive disease: a model for assigning a risk score. Tandem 2017.

44. Drobyski W. Results of a phase II clinical trial of tocilizumab, tacrolimus and methotrexate (TOC/TAC/MTX) for the prevention of acute graft versus host disease (GVHD) and matched case control comparison to TAC/MTX after allogeneic stem cell transplantation. Tandem 2017.

45. Ballen K. Excellent outcomes in 1589 patients receiving umbilical cord blood transplantation using unlicensed units from a centralized cord blood registry. Tandem

2017.

46. Holtan S. Follistatin and Endoglin: Potential Biomarkers of Endothelial Damage and Non-Relapse Mortality after Myeloablative Allogeneic Hematopoietic Cell Transplantation in Blood and Marrow Transplant Clinical Trials Network (BMT CTN) 0402. Tandem 2017.

47. Pidala J. Multi-state modeling identifies significant determinants of immune suppression discontinuation and risk for subsequent graft vs. host disease: A comprehensive secondary data analysis of BMT CTN 0201 and 0402 trials. Tandem 2017.

48. Godfrey J. Autologous (auto) versus matched sibling donor (MSD) or matched unrelated donor (MUD) allogeneic (allo) hematopoietic cell transplantation (HCT) in follicular lymphoma (FL) patients (pts) with early chemoimmunotherapy failure (ECF): A Center for International Blood and Marrow Transplant Research (CIBMTR) analysis. ASCO 2017.

49. Miller J. Excellent outcomes in 1589 patients receiving umbilical cord blood transplantation using unlicensed units from a centralized cord blood registry. EBMT 2017.

50. Lazaryn A. Prognostic significance of cytogenetic abnormalities in patients with Philadelphia-negative ALL undergoing allogeneic hematopoietic stem cell transplantation in complete remission: A CIBMTR analysis. ASH 2017.

51. Yeshurun M. Graft-vs-leukemia effect in acute lymphoblastic leukemia: mild acute Graft-vs-Host disease protects against relapse and improves survival after allogeneic transplantation: A CIBMTR analysis. ASH 2017.

52. Brown J. Prognostic score and cyteogenetic risk classification for chronic lymphocytic leukemia patients who underwent reduced intensity conditioning allogeneic HCT: A CIBMTR report. ASH 2017.

53. Chhabra S. Comparison of outcomes after myloablative versus reduced intensity conditioning allogeneic hematopoietic cell transplantation for chronic myeloid leukemia. ASH 2017.

54. Hu B. Optimal timing of allogeneic stem cell transplantation for chronic myeloid leukemia patients in the tyrosine kinase inhibitor era. ASH 2017.

55. Prokopishyn N. Bone marrow transplant product quality has decreased over time. A retrospective examination of NMDP collected bone marrow products from 1994-2016.

ASH 2017.

56. Fuchs E. Selecting between HLA-matched siblings and HLA-haploidentical related donors for acute leukemia in the era of post-transplant cyclophosphamid: The CIBMTR and Acute Leukemia Aorking party of the EBMT. ASH 2017.

57. Mehta R. Graft-versus-Host disease free relapse free survival and chronic GVHD in alternative donor hematopoietic cell transplantation in pediatric patients. ASH 2017.

58. Mehta R. Graft-versus-Host disease free relapse free survival and chronic GVHD in alternative donor hematopoietic cell transplantation in adults. ASH 2017.

59. Shaw B. Analysis of 10,462 8/8 HLA-matched unrelated donor transplants could not identify a donor selection score, as younger age is the only significant donor characteristic associated with survival. ASH 2017.

60. Gadalla S. Chromosome 6 loss of heterozygosity in pre-transplant blood samples of patients with severe aplastic anemia is associated with lower risk of acute GVHD. ASH 2017.

61. Gadalla S. Donor lymphocyte cell-specific telomere length and causes of death after unrelated hematopoietic cell transplant in patients with marrow failure. ASH 2017.

62. Norkin M. Late fetal infections remain higher than expected in adults receiving allogeneic stem cell transplant. ASH 2017.

63. Norkin M. Late fetal infections remains frequent cause of mortality in pediatric allogeneic stem cell transplant recipients. ASH 2017.

64. Kumar S. Revised-international staging system is independently predictive and prognostic for early relapse after upfront autologous hematopoietic cell transplantation for newly diagnosed multiple myeloma. ASH 2017.

65. Kumar S. A comparison between 3 staging systems in multiple myeloma using the center for international blood and marrow transplant research database. ASH 2017.

66. Eikema R. Allogeneic hematopoietic stem cell transplantation in older patients aged 50 or older with severe aplastic anaemia: results from the european society for blood and marrow transplant and the center for international blood and marrow transplant research. ASH 2017.

67. Brunstein C. The effect of conditioning regimen dose reduction in obese patients undergoing autologous transplantation. ASH 2017.

68. Majhail N. Individualized treatment summaries and survivorship care plans for hematopoietic cell transplant survivors reduces cancer treatment distress in a randomized multicenter study. ASH 2017.

69. Medac. Allogeneic hematopoietic cell transplantation for acute myeloid leukemia and myelodysplastic syndrome: effect of transplant conditioning regimen intensity on outcomes. ASH 2017.

70. Denzen E. Healthcare reimbursement and service utilization for one year of post-allogeneic hematopoietic cell transplantation care for medicare beneficiaries ages 65 and older with acute myeloid leukemia. ASH 2017.

71. Murphy E. Individualized treatment summaries and survivorship care plans for hematopoietic cell transplant survivors reduces cancer treatment distress in a randomized multicenter study. ASH 2017.

72. El-Jawahri A. What do transplant physicians think about palliative care? A national survey study. ASH 2017.

73. Horowitz M. Nicord single unit expanded umbilical cod bblood transplantation: Final results of a multicenter Phase I/II trual. ASH 2017.

74. Halagan M, Eapen M, Shaw B, et al. Selecting Optimal Cord Blood Units: The Limitations of Cell Dose. ASH 2017.

75. Halagan M, Wang W, Bashyal P, et al. GFE ACT: A Community Resource for Calling HLA Allele Names from Consensus Sequences with Gene Feature Enumeration Notation. ASHI 2017.

76. Maiers M, Louzoun Y, Pymm P, et al. Machine learning model that predicts binding between KIR3DL1 and HLA Class I allotypes. ASHI 2017.

77. Wei W. MIHAIP: Comprehensive pipeline to discover immunogenic minor histocompatibility antigens via whole genome sequences of HLA-matched donor-recipient pairs. ASHI. 2017.

78. Maiers M, Halagan M, Wang W, et al. Community resources for automated annotation of HLA, KIR and beyond. EFI 2017.

79. Milius RP, Schneider J, Brown A, et al. HLA and the EMR: Developing HL7 FHIR tools for exchanging NGS-based HLA genotyping. EFI 2017.

80. Chhabra S. Graft-Versus-Host Disease (GVHD) Prophylaxis in Reduced Intensity Conditioning (RIC) Allogeneic Hematopoietic Cell Transplantation (alloHCT): Comparing the Efficacy of mycophenolate mofetil (MMF) and methotrexate (MTX) in combination with calcineurin inhibitor (CNI). Tandem 2018.

81. Hamilton B. Cyclosporine (CSA) in combination with Mycophenolate Mofetil (MMF) Leads to Increased incidence of Graft-versus-Host Disease (GVHD) and Inferior Outcomes after Myeloablative Allogeneic Hematopoietic Cell Transplantation (HCT): a Center for International Blood and Marrow Transplant Research (CIBMTR) analysis. Tandem 2018.

82. Hahn T. Genome-wide significant donor genetic associations with disease death in AML and MDS patients in the first 1 year after BMT are not modified by Conditioning Intensity or TBI. Tandem 2018.

83. Hahn T. Genetic Associations with Day +100 Transplant Related Mortality (TRM) after HLA-Matched Unrelated Donor (MUD) Blood and Marrow Transplantation (DISCOVeRY-BMT Study). Tandem 2018.

84. Wang Y. Clonal alterations and survival after unrelated donor allogeneic hematopoietic stem cell transplant in patients with Fanconi anemia. Tandem 2018.

85. Askar M. Analysis of Single Nucleotide Polymorphisms (SNP) Donor/Recipient Mismatches in the Gamma Block of the Major Histocompatibility Complex (MHC) And Their Association With Hematopoietic Cell Transplantation (HCT) Outcomes: A CIBMTR Study. Tandem 2018.

86. Paczesny S. Functional genetic variants of the ST2 gene for risk stratification of GVHD and TRM outcomes. Tandem 2018.

87. Knight J, Rizzo D, Cole S. Association of CTRA and socioeconomic status in URD HCT. Tandem 2018.

88. Bachanova V. Graft-versus-leukemia responses in chronic lymphocytic leukemia (CLL) are not influenced by natural killer cell (NK) KIR immunogenetics: a CIBMTR analysis. Tandem 2018.

89. Naik S. Outcomes of Allogeneic Hematopoietic Cell Transplants with EBV Positive or EBV Negative Post-Transplant Lymphoproliferative Disorder (PTLD). Tandem 2018.

90. Bhatt N. Survivors of Childhood Allogeneic Hematopoietic Cell Transplant Have Higher Unemployment Rates Compared to the General US Population. Tandem 2018.

91. Shah N. Outcome of Patients 65 Years and Older with Non-Hodgkin Lymphoma (NHL) Receiving Reduced-Intensity Conditioning Allogeneic Hematopoietic Stem Cell Transplantation Compared to Patients 55-64 Years of Age: A Center for International Bone Marrow Transplant Research (CIBMTR) Analysis. Tandem 2018.

92. Brogile L. Evaluation of the Hematopoietic Cell Comorbidity Index (HCT-CI) in Recipients of Allogeneic Transplantation for Non-Malignant Diseases. Tandem 2018.

93. Parikg S. Survival Trends after Allogeneic Hematopoietic Cell Transplant (HCT) in Children less than one-year-old (infants). Tandem 2018.

94. Zinter M. Improved Mortality Prognostication for Critically Ill Pediatric Hematopoietic Cell Transplant Patients: Results from a Virtual Pediatric Systems (VPS) and Center for International Blood and Marrow Transplant Research (CIBMTR) Database Merger. Tandem 2018.

95. Vanness D. Estimating Propensity Scores for the Receipt of Allogeneic Hematopoietic Cell Transplantation (AlloHCT) in Outcomes Research using Claims Data: A Machine Learning Approach. Tandem 2018.

96. El-Jawahri A. A National Survey Study of Transplant Physicians' Attitudes about Palliative Care. Tandem 2018.

97. Seftel M. Survey Of The Screening And Management For Clonal Disorders Of Hematopoiesis In Related Allogeneic Donors. EBMT 2018.

98. Louzoun Y, Litniski A, Madbouly A, et al. Single haplotype admixture models using large-scale HLA genotypes to reproduce human admixture. EFI 2018.

99. Bishara A, Halagan M, Crautbar C, et al. High resolution HLA-A, -B, -C, -DRB1 and –DQB1 allele and haplotype frequencies for Arab donors in the Hadassah bone marrow registry. EFI 2018.

100. Louzoun Y, Gragert L, Maiers M, et al. HLA Class I haplotype diversity is consistent with selection for frequent existing haplotypes. EFI 2018.

VIII. Acronyms

AABB	American Association of Blood Banks
AAFA	African American (NMDP race code)
AAR/IP	After Action Review/Improvement Plan
ABA	American Burn Association
ABD	Antigen Binding Domain
ABMTR	Autologous Blood and Marrow Transplant Registry
AC	Apheresis Center
ACT	Allele Calling Tool
AFA	African American
AFR	African
AFRRI	Armed Forces Radiobiology Research Institute
AGNIS®	A Growable Network Information System
AHA	American Hospital Association
AHLS	Advanced HAZMAT Life Support
AIM	Ancestry Informative Markers
AINDI	South Asian
AISC	American Indian South or Central
ALANAM	Alaska Native or Aleut
ALD	Asymmetric Linkage Disequilibrium
ALDH	Aldehyde Dehydrogenase
ALDHbr	Aldehyde Dehydrogenase bright
ALT-LOCI	Alternate Loci
AMIND	North American Indian
AML	Acute Myelogenous Leukemia

AMR	American Indian
ANSI	American National Standards Institute
APHIA	Asia Pacific Histocompatibility and Immunogenetics Association
API	Application Programming Interface
AQP	Ancestry Questionnaire Project
ARC GIS	ArcGIS is a brand name: GIS = Geographical Information System
ARD	Antigen Recognition Domain
ARRA	The American Recovery and Reinvestment Act of 2009
ARS	Acute Radiation Syndrome (also known as Acute Radiation Sickness)
ARS	Antigen Recognition Site
ASBMT	American Society for Blood and Marrow Transplantation
ASEATTA	Australian and South East Asian Tissue Typing Association
ASH	American Society for Histocompatibility
ASHG	American Society of Human Genetics
ASHI	American Society for Histocompatibility and Immunogenetics
ASI	Asian American
ASPR	Assistant Secretary for Preparedness and Response
ASTHO	Association of State and Territorial Health Officials
AUC	Area Under Curve
B-LCLs	B-Lymphocytic Cell Lines
B2B	Business to Business
BAA	Broad Agency Announcement
BARDA	Biomedical Advanced Research and Development Authority
BART	Bayesian Additive Regression Trees

BBMT	Biology of Blood and Marrow Transplantation
BCP	Business Continuity Planning
BCPeX	Business Continuity Plan Exercise
BFU-E	Burst Forming Unit-Erythrocytes
BGI	Beijing Genome Institute
BISC	Bioinformatics Integration Support Contract
BM	Bone Marrow
BMCC	Bone Marrow Coordinating Center
BMDW	Bone Marrow Donors Worldwide
BMT	Bone Marrow Transplant/Transplantation
BMT CTN	Blood and Marrow Transplant - Clinical Trials Network
BODI	Business Objects Data Integrator
BRAGG	Bioinformatics Research Advisory Ginger Group
BRIDG	Biomedical Research Integrated Domain Group
BRT	Basic Radiation Training
BTM	Be The Match
caBIG	NIH/NCI Cancer Biomedical Informatics Grid
caDSR	Cancer Data Standards Repository
C&A	Certification and Accreditation
CAP	College of American Pathologists
CARB	Black Caribbean
CARHIS	Caribbean Hispanic
CARIBI	Caribbean Indian
CATI	Computer Assisted Telephone Interviewing

CAU	Caucasian
C&A	Certification and Accreditation
CB	Cord Blood
CBA	Cord Blood Association
CBAG	Cord Blood Advisory Group
CBITT	Center for Biomedical Informatics and Information Technology
CBMTG	Canadian Blood and Marrow Transplant Group
CBB	Cord Blood Bank
CBC	Congressional Black Caucus
CBS	Canadian Blood Service
CBT	Cord Blood Transplantation
CBU	Cord Blood Unit
CC	Collection Center
CCD	Continuity of Care Document
CD	Cluster of Differentiation
CDA	Clinical Document Architecture
CDC	Centers for Disease Control
CFU	Colony Forming Unit
CDE	Common Data Elements
CDISC	Clinical Data Interchange Standards Consortium
CEM	Certified Emergency Manager
CEO	Chief Executive Officer
CFO	Chief Financial Officer
CEP	Collect Eject Protect

CFU	Colony Forming Unit
CFU-GM	Colony Forming Unit-Granulocyte Macrophage
CFU-GEMM	Colony Forming Unit-Gran Erythrocyte Macrophage Monocyte
CG-WG	Clinical Genomics Work Group
cGy	CentiGrey
CHORI	Children's Hospital of Oakland Research Institute
CHOP	The Children's Hospital of Philadelphia
CHS	Certified Histocompatibility Specialist
CHTC	Certified Hematopoeitic Transplant Coordinator
CI	Confidence Interval
CIBMTR®	Center for International Blood & Marrow Transplant Research
CIO	Chief Information Officer
CIT	CIBMTR Information Technology
CLIA	Clinical Laboratory Improvement Amendment
CMCR	Centers for Medical Countermeasures Against Radiation
CMDP	China Marrow Donor Program
CME	Continuing Medical Education
CMF	Community Matching Funds
CML	Chronic Myelogenous Leukemia
CMO	Chief Medical Officer
CMS	Center for Medicare and Medicaid Services
CMV	Cytomegalovirus
CNV	Copy Number Variation
COG	Children's Oncology Group

ConRad	German Conference on Radiation
CPA	Center Performance Analytics
CPI	Continuous Process Improvement
CREG	Cross Reactive Groups
CRF	Case Report Forms
CRI	Complete Remission
CRID	CIBMTR Recipient ID
CRIS	Computerized Repository Inventory System
CRO	Chief Recruitment Officer
CSF	Colony Stimulating Factors
CSO	Chief Strategy Officer
CSS	Center Support Services
CSS	Custom Search Support
CT	Confirmatory Testing
CTA	Clinical Trial Application
CTLp	Cytotoxic T Lymphocyte Precursor
CTMS	Clinical Trial Management System
CUPC	Cisco Unified Personal Communicator
CV	Co-efficient of Variations
CWD	Common Well Documented
DAIT	Division of Allergy, Immunology, and Transplantation
DaSH	Data Standards Hackathon
DC	Donor Center
DCAA	Defense Contract Audit Agency

DFCI	Dana-Farber Cancer Institute
DFS	Disease Free Survival
DHHS	Department of Health and Human Services
DIY	Do It Yourself
DKMS	Deutsche Knochenmarkspenderdatei
DMSO	Dimethylsulphoxide
DNA	Deoxyribonucleic Acid
DoD	Department of Defense
DOE	Department of Energy
DP	Domain Prediction
DQ	Data Quality
DR	Disaster Recovery
D/R	Donor/Recipient
DRPP	Donor Related Pair Project
DSA	Donor specific anti-HLA antibody
DSMB	Data Safety Monitoring Board
DSTU	Draft Standard for Trial Use
DVD	Digital Video Disc
EBMT	European Group for Blood and Marrow Transplantation
EC	Ethics Committee
ED	Emergency Department
eDBiC	Enhanced Data Back to Centers
EDC	Electronic Data Capture
EFI	European Federation for Immunogenetics

EHR	Electronic Health Record
ELISA	Enzyme-linked Immunosorbent Assay
ELIspot	Enzyme-linked Immunosorbent Spot
EM	Expectation Maximization
EMDIS	European Marrow Donor Information System
EMR	Electronic Medical Records
EMS	Emergency Medical System
ENS	Emergency Notification System
ERSI	Environment Remote Sensing Institute
ESRI	Environmental Systems Research Institute
eTMF	electronic Trial Master File
EUR	European American
E-utilities	Entrez Programming Utilities
FACS	Fluorescent Activated Cell Sorting
FBI	Federal Bureau of Investigation
FDA	Food and Drug Administration
FDR	Fund Drive Request
FGM	***France*** Greffe de Moelle
FHCRC	Fred Hutchinson Cancer Research Center
FHIR	Fast Healthcare Interoperability Resources
FILII	Filipino
FLOCK	Flow Cytometry Analysis Component
FN	FormsNet
FN3	FormsNet3

Fst	Fixation Index
FWA	Federal-wide Assurance
FY	Fiscal Year
GEMM	Granulocyte, Erythrocyte, Monocyte/macrophage, Megakaryocyte
GETS	Government Emergency Telecommunications Service
GCSF	Granulocyte-Colony Stimulating Factor (also known as filgrastim)
GDRGEN	Group (HLA)-DR Generic
GETS	Government Emergency Telecommunication Service
GFE	Gene Feature Enumeration
GIS	Geographic Information System
GL	Genotype List
GM	Granulocyte Macrophage
GM-CSF	Granulocyte Macrophage Colony Stimulating Factor
GS	General Services
GTR	Genetic Testing Registry
GUI	Graphical User Interface
GVHD	Graft vs. Host Disease
GVL	Graft-Versus-Leukemia
GWAS	Genome Wide Association Studies
GWASH	Genome-Wide Association Scan for Histocompatibility Antigens
Gy	Gray-measure of dose of irradiation
HAPI	HL7 Application Programming Interface
HARPs	HLA Ambiguity Resolution Primers
HAWI	Hawaiian or other Pacific Islander Unspecified

HAZMAT	Hazardous Material
HBCU	Historical Black Colleges and University
HC	Hematopoietic Cell
HCS®	Health Care Standard
HCT	Hematopoietic Cell Transplantation
HRQoL	Health Related Quality of Life
HEPP	Hospital Emergency Preparedness Program
HHQ	Health History Questionnaire
HHS	Health and Human Services
HIEDFS	HLA Information Exchange Data Format Standards
HIPAA	Health Insurance Portability and Accountability Act
HIS	Hispanic
HIV	Human Immunodeficiency Virus
HLA	Human Leukocyte Antigen
HML	Histoimmunogenetics Mark-up Language
HR	High Resolution
HRSA	Health Resources and Services Administration
HSC	Hematopoietic Stem Cell
HSCT	Hematopoietic Stem Cell Transplant
HSR	Health Services Research
HTML	HyperText Markup Language
HUGO	Human Genome Organization
HWE	Hardy-Weinberg Equilibrium
IBMDR	Italian Bone Marrow Donor Registry

IBMTR	International Bone Marrow Transplant Registry
IBWC	Immunobiology Working Committee
ICRHER	International Consortium for Research on Health Effects of Radiation
ID	Identification
IDAWG	Immunogenetics Data Analysis Working Group
IDM	Infectious Disease Markers
IDS	Integrated Data Store
IDW	Integrated Data Warehouse
Ig	Immunoglobulin
IHIW	International Histocompatibility and Immunogenetics Workshop
IHIWS	International Histocompatibility Work Shop
IHWG	International Histocompatibility Working Group
IIDB	Immunobiology Integration Database
IIMMS	International Immunomics Society
IMGT	ImMunoGeneTics
IMStrategy	Information Management Strategy
ImmPort	Immunology Database and Analysis Portal
IND	Investigational New Drug
IND	Improvised Nuclear Device
IPD	Immuno Polymorphism Database
IPR	Immunobiology Project Results
IRB	Institutional Review Board
IS	Information Services
ISO	International Organization for Standardization

IT	Information Technology
JAPI	Japanese
JCHO	Joint Commission of Healthcare Organizations
JCAHO	Joint Commission on Accreditation of Healthcare Organizations
JMML	Juvenile Myelomonocytic Leukemia
KIR	Killer Immunoglobulin-like Receptor
KORI	Korean
KT	Kiloton
LD	Linkage Disequilibrium
LEL	Low Expression Alleles
LOINC	Logical Observation Identifiers Names and Codes
LSSG	Life Sciences Strategy Group
LTA	Lymphotoxin Alpha
M	Million
MALDI-TOF	Matrix-Assisted Laser Desorption/Ionization – Time Of Flight
MBS	Masters of Biological Science
MCW	Medical College of Wisconsin
MD	Medical Doctor
MDACC	MD Anderson Cancer Center
MDHT	Model Driven Health Tools
MDS	Myelodysplastic Syndrome
MENAFC	MidEast/North Coast of Africa
MG	Predicted Match Grades
mHAg	Minor Histocompatibility Antigen

MHC	Major Histocompatibility Complex
MICA	MHC Class I-Like Molecule, Chain A
MICB	MHC Class I-Like Molecule, Chain B
MiHAs	Minor Hitocompatibility Antigens
MIRING	Minimal Information for Reporting Immunogenomic NGS Genotyping
MKE	Milwaukee
MLC	Mixed Lymphocyte Culture
MLR	Mixed loss Ratio
MOU	Memorandum of Understanding
MRD	Minimal Residual Disease
MSD	Matched Sibling Donor
MSKCC	Memorial Sloan-Kettering Cancer Center
MSP	Minneapolis
MSWHIS	Mexican or Chicano
MUD	Matched Unrelated Donor
NAC	Nuclear Accident Committee
NACCHO	National Association of County and City Health Officials
NAM	Native American
NAMER	North American
NARR	National Alliance for Radiation Readiness
NCBI	National Center for Biotechnology Information
NCBM	National Conference of Black Mayors
NCHI	Chinese
NCI	National Cancer Institute

NDMS	National Disaster Medical System
NECEP	New England Center for Emergency Preparedness
NEMO	N-locus Expectation-Maximization using Oligonucleotide typing data
NGS	Next Generation Sequencing
NHLBI	National Heart Lung and Blood Institute
NIAID	National Institute of Allergy and Infectious Diseases
NIH	National Institutes of Health
NIMA	Non-inherited maternal antigen
NIMS	National Incident Management System
NK	Natural Killer
NL	Netherlands
NLE	National Level Exercise
NLM	National Library of Medicine
NMDP®	National Marrow Donor Program
NNSA	National Nuclear Security Administration
NRP	National Response Plan
NST	Non-myeloablative Allogeneic Stem Cell Transplantation
NYC	New York City
OB	Obstetrician
OB/GYN	Obstetrics & Gynecology
OBIEE	Oracle Business Intelligence Enterprise Edition
OCP	Operational Continuity Planning
OCR/ICR	Optical Character Recognition/Intelligent Character Recognition
OHRP	Office of Human Research Protections

OIT	Office of Information Technology
OMB	Office of Management and Budget
ONR	Office of Naval Research
OPA	Office of Patient Advocacy
ORP	Operational Resiliency Plan
OS	Overall Survival
P2P	Peer-to-Peer
PA	Presence/Absence
PBMC	Peripheral Blood Mononuclear Cells
PBSC	Peripheral Blood Stem Cell
PCR	Polymerase Chain Reaction
PED	Pedigree
PHYCuS	Public Haplotype Frequency Curation Service
PI	Principle Investigator
POI	Procedures of Interaction
PP	Psudopatient
PRO	Patient Reported Outcomes
PROMIS®	Patient-Reported Outcomes Measurement Information System
PSA	Public Service Announcement
PT	Proficiency Testing
QAMS	Quality Assurance Membership Services
QARM	Quality Assurance and Risk Management
QC	Quality control
QR	Quick Response

R	Race Pair
R&D	Research and Development
RCC	Renal Cell Carcinoma
RCI	Resource for Clinical Investigations
RCI BMT	Resource for Clinical Investigation in Blood and Marrow Transplantation
RD Safe	Related Donor Safety
REAC/TS	Radiation Emergency Assistance Center/Training Site
RED	Radiological Exposure Devices
REDMO	Spanish Bone Marrow Donor Registry
REMM	Radiation Event Medical Management
REMPAN	Radiation Emergency Medical Preparedness and Assistance
REST	Representational State Transfer
RFA	Request for Application
RFI	Request for Information
RFP	Request for Proposal
RFQ	Request for Quotation
RG	Recruitment Group
Rh	Rhesus
RITN	Radiation Injury Treatment Network
ROC	Receiver Operating Characteristics
RSSA	R-Shiny Search Application
RT-PCR	Reverse Transcriptase-Polymerase Chain Reaction
SAA	Severe Aplastic Anemia
SAP	Single Amino-Acid Polymorphisms

SBT	Sequence Based Typing
SCAHIS	South/Central American Hispanic
SCAMB	Black South or Central America
SCD	Sickle Cell Disease
SCSEAI	Southeast Asian
SCT	Stem Cell Transplantation
SCTOD	Stem Cell Therapeutics Outcome Database
SEARCH	Page 10
SFVT	Sequence Feature Variant Type
SG	Sample Group
SHF	Synthetic Haplotype Frequency
SIRE	Self Identified Race and Ethnicity
SLCBB	St. Louis Cord Blood Bank
SLW	STAR Link® Web
SMRT	Single Molecule, Real-Time
SNOMED CT	Systematized Nomenclature of Medicine – Clinical Terms
SNP	Single Nucleotide Polymorphism
SNS	Strategic National Stockpile
SO	Sequence Ontology
SOA	Service Oriented Architecture
SOP	Standard Operating Procedure
SQL	Structured Query Language
SRA	Sequence Read Archive
SRB	Survey Research Group

SRG	Survey Research Group
SSA	Search Strategy Advice
SSO	Sequence Specific Oligonucleotides
SSP	Sequence Specific Primers
SSOP	Sequence Specific Oligonucleotide Probes
SSRS	Sample Storage Research Study
STAR®	Search, Tracking and Registry
STaT	Selection, Typing and Transplant
SVM	Support Vector Machine
SWOG	Southwest Oncology Group
TBI	Total Body Irradiation
TC	Transplant Center
TCE	T-cell Epitope
TCR	T-cell Receptor
TCSA	Transplant Center Specific Analysis
TED	Transplant Essential Data
TNC	Total Nucleated Cell
TNCC	Total Nucleated Cell Count
TRM	Transplant Related Mortality
TRS	Typing Resolution Score
TSA	Transportation Security Agency
TTY	Text Telephone
TU	Temporarily Unavailable
UCB	Umbilical Cord Blood

UCBT	Umbilical Cord Blood Transplant
UCSF	University of California – San Francisco
UI	User Interface
UML	Unified Modeling Language
UNK	Unkown
URD	Unrelated Registry Donor
US	United States
USAID	United States Agency for International Development
USID	Unique System Identifier
USIDNet	US Immunodeficiencies Network
USB	Universal Serial Bus
UTR	Untranslated Region
VCF	Variant Call Format
VIET	Vietnamese
VP	Vice President
VPN	Virtual Private Network
WBMT	Worldwide Network for Bone Marrow Transplantation
WC	Working Committees
WebEOC®	Web-based Emergency Operations Center
WGA	Whole Genome Amplification
WH	White
WHO	World Health Organization
WMDA	World Marrow Donor Association
WU	Work-up

XML	Extensible Markup Language
ZKRD	Zertrales Knochenmarkspender – Register für die Bundesrepublik Deutchland
7 AAD	7-Aminoactinomycin D